Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:sssptal635jxs

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * * * Welcome to STN International * * * * * * * * * *

NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2		"Ask CAS" for self-help around the clock
NEWS 3	May 10	PROUSDDR now available on STN
NEWS 4	May 19	PROUSDDR: One FREE connect hour, per account, in both May and June 2004
NEWS 5	May 12	EXTEND option available in structure searching
NEWS 6	May 12	Polymer links for the POLYLINK command completed in REGISTRY
NEWS 7	May 17	FRFULL now available on STN
NEWS 8	May 27	New UPM (Update Code Maximum) field for more efficient patent SDIs in CAplus
NEWS 9	May 27	CAplus super roles and document types searchable in REGISTRY
NEWS 10	May 27	Explore APOLLIT with free connect time in June 2004
NEWS 11	Jun 22	STN Patent Forums to be held July 19-22, 2004
NEWS 12	Jun 28	Additional enzyme-catalyzed reactions added to CASREACT
NEWS 13	Jun 28	ANTE, AQUALINE, BIOENG, CIVILENG, ENVIROENG, MECHENG, and WATER from CSA now available on STN(R)

NEWS EXPRESS	MARCH 31 CURRENT WINDOWS VERSION IS V7.00A, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 26 APRIL 2004
NEWS HOURS	STN Operating Hours Plus Help Desk Availability
NEWS INTER	General Internet Information
NEWS LOGIN	Welcome Banner and News Items
NEWS PHONE	Direct Dial and Telecommunication Network Access to STN
NEWS WWW	CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that specific topic.

All use of STN is subject to the provisions of the STN Customer agreement. Please note that this agreement limits use to scientific research. Use for software development or design or implementation of commercial gateways or other similar uses is prohibited and may result in loss of user privileges and other penalties.

* * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 11:57:47 ON 01 JUL 2004

=> FIL MEDLINE BIOSIS EMBASE CA SCISEARCH
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 11:57:54 ON 01 JUL 2004

FILE 'BIOSIS' ENTERED AT 11:57:54 ON 01 JUL 2004

```
FILE 'EMBASE' ENTERED AT 11:57:54 ON 01 JUL 2004
COPYRIGHT (C) 2004 Elsevier Inc. All rights reserved.

FILE 'CA' ENTERED AT 11:57:54 ON 01 JUL 2004
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'SCISEARCH' ENTERED AT 11:57:54 ON 01 JUL 2004
COPYRIGHT 2004 THOMSON ISI

=> s polymerase?
L1      949985 POLYMERASE?

=> s ((non (n) eu!aryot?) or pro!aryot?) (2n) l1
L2         760 ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (2N) L1

=> s ((non (n) eu!aryot?) or pro!aryot?) (s) l1
L3        2599 ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1

=> s (((non (n) eu!aryot?) or pro!aryot?)) (s) l1) or T3 ot T7 or SP6
UNMATCHED RIGHT PARENTHESIS 'L6) OR'
The number of right parentheses in a query must be equal to the
number of left parentheses.

=> s ((non (n) eu!aryot?) or pro!aryot?)) (s) l1) or T3 ot T7 or SP6
UNMATCHED RIGHT PARENTHESIS 'RO!ARYOT?)) '
The number of right parentheses in a query must be equal to the
number of left parentheses.

=> s ((non (n) eu!aryot?) or pro!aryot?) (s) l1) or T3 ot T7 or SP6
UNMATCHED RIGHT PARENTHESIS 'L6) OR'
The number of right parentheses in a query must be equal to the
number of left parentheses.

=> s (((non (n) eu!aryot?) or pro!aryot?) (s) l1) or T3 ot T7 or SP6
L4        5927 (((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1) OR T3 OT T7 OR SP6

=> s (((non (n) eu!aryot?) or pro!aryot? or bacter?) (s) l1) or T3 ot T7 or SP6
L5       32470 (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) (S) L1) OR T3
               OT T7 OR SP6

=> s l5 (s) intron?
L6         275 L5 (S) INTRON?

=> s l5 (2) intron?
MISSING OPERATOR 'L30 (2'
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s l5 (2N) intron?
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L25 (2A) INTRON?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L26 (2A) INTRON?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L27 (2A) INTRON?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L28 (2A) INTRON?'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L29 (2A) INTRON?'
L7         448 L5 (2N) INTRON?
```

```
=> s l5 (N2) intron?
MISSING OPERATOR 'L30 (N2'
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> dup rem l6
PROCESSING COMPLETED FOR L6
L8          131 DUP REM L6 (144 DUPLICATES REMOVED)

=> s l8 and Py<=1997
   2 FILES SEARCHED...
L9          74 L8 AND PY<=1997

=> d l9 ibib abs 1-5

L9   ANSWER 1 OF 74     MEDLINE on STN
ACCESSION NUMBER:   97330447     MEDLINE
DOCUMENT NUMBER:    PubMed ID: 9186906
TITLE:              The acid lipase gene family: three enzymes, one highly
                    conserved gene structure.
AUTHOR:             Lohse P; Lohse P; Chahrokh-Zadeh S; Seidel D
CORPORATE SOURCE:   Department of Clinical Chemistry, Grosshadern Clinic,
                    University of Munich, Germany.
SOURCE:             Journal of lipid research, (1997 May) 38 (5)
                    880-91.
                    Journal code: 0376606. ISSN: 0022-2275.
PUB. COUNTRY:       United States
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        199707
ENTRY DATE:         Entered STN: 19970812
                    Last Updated on STN: 19970812
                    Entered Medline: 19970729
AB   Human gastric lipase (HGL; triacylglycerol lipase; EC 3.1.1.3) plays an
     important role in the digestion of dietary triglycerides in the
     gastrointestinal tract, especially in patients suffering from pancreatic
     lipase deficiencies. The enzyme is secreted by the fundic mucosa of the
     stomach and hydrolyzes the ester bonds of triglycerides under acidic pH
     conditions, while cholesteryl esters are not attacked. The 379-amino acid
     protein is highly homologous to two other acidic lipases, rat lingual
     lipase (RLL; triacylglycerol lipase; EC 3.1.1.3) and human lysosomal acid
     lipase (HLAL; cholesteryl esterase; EC 3.1.1.13). To determine whether
     this remarkable similarity is also present at the genomic level, we have
     elucidated the respective gene structures by screening three
     bacteriophage lambda libraries and by polymerase chain
     reaction-based intron amplification. The genes encoding HGL,
     RLL, and HLAL are composed of 10 exons interrupted by nine introns and
     span about 14 kb, 18.7 kb, and 38.8 kb of genomic DNA, respectively. The
     HGL and RLL gene organizations are identical, suggesting that RLL is the
     rat gastric lipase expressed in the serous von Ebner glands of the tongue.
     The positions of the HLAL intervening sequences are also absolutely
     conserved, except for the location of intron 1. Our results support the
     concept that HLAL and HGL/RLL are members of a gene family of lipases that
     most likely have evolved by duplication of an ancestral gene and
     subsequently assumed distinct roles in neutral lipid metabolism due to
     sequence divergence and different expression patterns.

L9   ANSWER 2 OF 74     MEDLINE on STN
ACCESSION NUMBER:   96152651     MEDLINE
DOCUMENT NUMBER:    PubMed ID: 8565067
TITLE:              Beyond homing: competition between intron endonucleases
                    confers a selective advantage on flanking genetic markers.
AUTHOR:             Goodrich-Blair H; Shub D A
```

CORPORATE SOURCE: Department of Biological Sciences, State University of New York at Albany 12222, USA.
CONTRACT NUMBER: GM37746 (NIGMS)
SOURCE: Cell, **(1996 Jan 26)** 84 (2) 211-21.
Journal code: 0413066. ISSN: 0092-8674.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199603
ENTRY DATE: Entered STN: 19960315
Last Updated on STN: 19980206
Entered Medline: 19960301

AB The closely related B. subtilis **bacteriophages** SPO1 and SP82 have similar **introns** inserted into a conserved domain of their DNA **polymerase** genes. These introns encode endonucleases with unique properties. Other intron-encoded "homing" endonucleases cleave both strands of intronless DNA; subsequent repair results in unidirectional gene conversion to the intron-containing allele. In contrast, the enzymes described here cleave one strand on both intron-containing and intronless targets at different distances from their common intron insertion site. Most surprisingly, each enzyme prefers DNA of the heterologous phage. The SP82-encoded endonuclease is responsible for exclusion of the SPO1 intron and flanking genetic markers from the progeny of mixed infections, a novel selective advantage imparted by an intron to the genome in which it resides.

L9 ANSWER 3 OF 74 MEDLINE on STN
ACCESSION NUMBER: 95023117 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7937082
TITLE: The DNA **polymerase** genes of several HMU-**bacteriophages** have similar group I **introns** with highly divergent open reading frames.
AUTHOR: Goodrich-Blair H; Shub D A
CORPORATE SOURCE: Department of Biological Sciences, University at Albany, SUNY 12222.
CONTRACT NUMBER: GM37746 (NIGMS)
SOURCE: Nucleic acids research, **(1994 Sep 11)** 22 (18) 3715-21.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M37686; GENBANK-U04812; GENBANK-U04813
ENTRY MONTH: 199411
ENTRY DATE: Entered STN: 19941222
Last Updated on STN: 19980206
Entered Medline: 19941103

AB A previous report described the discovery of a group I, self-splicing **intron** in the DNA **polymerase** gene of the Bacillus subtilis **bacteriophage** SPO1 (1). In this study, the DNA polymerase genes of three close relatives of SPO1: SP82, 2C and phi e, were also found to be interrupted by an intron. All of these introns have group I secondary structures that are extremely similar to one another in primary sequence. Each is interrupted by an open reading frame (ORF) that, unlike the intron core or exon sequences, are highly diverged. Unlike the relatives of Escherichia coli bacteriophage T4, most of which do not have introns (2), this intron seems to be common among the relatives of SPO1.

L9 ANSWER 4 OF 74 MEDLINE on STN
ACCESSION NUMBER: 94198233 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8148326

TITLE: Transcriptional regulation of immunoglobulin gene expression by anti-Ig.
AUTHOR: Johansson K; Sigvardsson M; Leanderson T
CORPORATE SOURCE: Immunology Unit, University of Lund, Sweden.
SOURCE: International immunology, **(1994 Jan)** 6 (1) 41-8.
Journal code: 8916182. ISSN: 0953-8178.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199405
ENTRY DATE: Entered STN: 19940523
Last Updated on STN: 19980206
Entered Medline: 19940509

AB When transfected into mouse splenic B cells stimulated with lipopolysaccharide (LPS) the expression of DNA vectors containing the chloramphenicol acetyl transferase gene under the control of a **SP6** kappa promoter and the Ig heavy chain **intron** enhancer could be down-regulated 5- to 10-fold by treatment of the cells with anti-Ig prior to transfection. Exchanging the SP6 kappa promoter by minimal promoters consisting of an octamer or a SP1 motif linked to TATA box did not impair the anti-Ig induced down-regulation while inserting a rabbit beta-globin promoter did. The transcriptional regulation could be observed after replacing the Ig heavy chain intron enhancer with a SV40 enhancer, or duplicated minimal Ig heavy chain enhancers containing or lacking the octamer element. The down-regulation was not dependent on the level of transcriptional stimulation observed. A difference in Oct2 expression could neither be detected at the RNA nor protein level after treatment of LPS stimulated B cells with anti-Ig or phorbol-dibutyrate. Anti-Ig treatment, but not phorbol-di-butyrate treatment, induced increased levels of AP1 and NF kappa B transcription factors. Thus, either differentiation specific transcriptional control of Ig genes is exerted via transcription factors common to several distinct enhancers or via transcriptional adaptor molecules that can interact with several distinct DNA binding proteins.

L9 ANSWER 5 OF 74 MEDLINE on STN
ACCESSION NUMBER: 92380475 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1324872
TITLE: The DNA polymerase-encoding gene of Bacillus subtilis bacteriophage SPO1.
AUTHOR: Scarlato V; Gargano S
CORPORATE SOURCE: International Institute of Genetics and Biophysics, Naples, Italy.
SOURCE: Gene, **(1992 Sep 1)** 118 (1) 109-13.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M74891; GENBANK-M74892; GENBANK-M79309; GENBANK-M79310; GENBANK-M84415; GENBANK-M88536; GENBANK-M88537; GENBANK-M88538; GENBANK-M88539; GENBANK-M90357
ENTRY MONTH: 199209
ENTRY DATE: Entered STN: 19921018
Last Updated on STN: 19921018
Entered Medline: 19920928

AB The **bacteriophage** SPO1 DNA **polymerase**-encoding gene, which contains a self-splicing **intron**, has been sequenced and its amino acid (aa) sequence has been deduced. The aa sequence of SPO1 DNA polymerase shows a high degree of similarity with that of DNA polymerase I from Escherichia coli (PolI). Alignment with the sequences of PolI, and the phi 29 and SPO1 DNA polymerases indicate that the aa

residues that have been implicated in 3'----5' exonuclease activities are conserved.

=> d his

(FILE 'HOME' ENTERED AT 11:57:47 ON 01 JUL 2004)

FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 11:57:54 ON 01 JUL 2004

```
L1        949985 S POLYMERASE?
L2           760 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (2N) L1
L3          2599 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1
L4          5927 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1) OR T3 OT T7 OR S
L5         32470 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) (S) L1) OR T3
L6           275 S L5 (S) INTRON?
L7           448 S L5 (2N) INTRON?
L8           131 DUP REM L6 (144 DUPLICATES REMOVED)
L9            74 S L8 AND PY<=1997
```

=> s l5 and (intron (3n) (introduc? or non (2n) nativ?) or insert? or spliced)
L10 2322 L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT? OR SPLICED)

=> d l10 1-10 ibib abs

L10 ANSWER 1 OF 2322 MEDLINE on STN
ACCESSION NUMBER: 2004295436 IN-PROCESS
DOCUMENT NUMBER: PubMed ID: 15196018
TITLE: Altering DNA Polymerase Incorporation Fidelity by Distorting the dNTP Binding Pocket with a Bulky Carcinogen-Damaged Template.
AUTHOR: Yan S Frank; Wu Min; Geacintov Nicholas E; Broyde Suse
CORPORATE SOURCE: Departments of Chemistry and Biology, New York University, New York, New York 10003.
SOURCE: Biochemistry, (2004 Jun 22) 43 (24) 7750-65.
Journal code: 0370623. ISSN: 0006-2960.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-DATA-REVIEW; IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20040616
Last Updated on STN: 20040616

AB Fidelity of DNA polymerases is predominantly governed by an induced fit mechanism in which the incoming dNTP in the ternary complex fits tightly into a binding pocket whose geometry is determined by the nature of the templating base. However, modification of the template with a bulky carcinogen may alter the dNTP binding pocket and thereby the polymerase incorporation fidelity. High fidelity DNA **polymerases**, such as **bacteriophage** T7 DNA **polymerase**, are predominantly blocked by bulky chemical lesions on the template strand during DNA replication. However, some mutagenic bypass can occur, which may lead to carcinogenesis. Experimental studies have shown that a DNA covalent adduct derived from (+)-anti-BPDE [(+)-(7R,8S,9S,10R)-7,8-dihydroxy-9,10-epoxy-7,8,9,10-tetrahydrobenzo[a]pyrene], a carcinogenic metabolite of benzo[a]pyrene (BP), primarily blocks Sequenase 2.0, an exo(-)() T7 DNA polymerase; however, a mismatched dATP can be preferentially **inserted** opposite the damaged adenine templating base within the active site of the polymerase [Chary, P., and Lloyd, R. S. (1995) Nucleic Acids Res. 23, 1398-1405]. The goal of this work is to elucidate structural features that contribute to DNA polymerase incorporation fidelity in the presence of this bulky covalent adduct and to interpret the experimental findings on a molecular level. We have carried out molecular modeling and molecular dynamics simulations with AMBER 6.0,

investigating a T7 DNA polymerase primer-template closed ternary complex containing this 10S (+)-trans-anti-[BP]-N(6)-dA adduct in the templating position within the polymerase active site. All four incoming dNTPs were studied. The simulations show that the BP ring system fits well into an open pocket on the major groove side of the modified template adenine with anti glycosidic bond conformation, without disturbing critical polymerase-DNA interactions. However, steric hindrance between the BP ring system and the primer-template DNA causes displacement of the modified template adenine, so that the dNTP base binding pocket is enlarged. This alteration can explain the experimentally observed preference for incorporation of dATP opposite this lesion. These studies also rationalize the observed lower probabilities of incorporation of the other three nucleotides. Our results suggest that the differences in incorporation of dGTP, dCTP, and dTTP are due to the effects of imperfect geometric complementarity. Thus, the simulations suggest that altered DNA polymerase incorporation fidelity can result from adduct-induced changes in the dNTP base binding pocket geometry. Furthermore, plausible structural explanations for the observed effects of [BP]-N(6)-dA adduct stereochemistry on the observed stalling patterns are proposed.

L10 ANSWER 2 OF 2322 MEDLINE on STN
ACCESSION NUMBER: 2004292884 IN-PROCESS
DOCUMENT NUMBER: PubMed ID: 15194191
TITLE: Evolution of **bacterial** RNA **polymerase**: implications for large-scale **bacterial** phylogeny, domain accretion, and horizontal gene transfer.
AUTHOR: Iyer Lakshminarayan M; Koonin Eugene V; Aravind L
CORPORATE SOURCE: National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD 20894, USA.
SOURCE: Gene, (2004 Jun 23) 335 73-88.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-DATA-REVIEW; IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20040615
Last Updated on STN: 20040615

AB Comparative analysis of the domain architectures of the beta, beta', and sigma(70) subunits of **bacterial** DNA-dependent RNA **polymerases** (DdRp), combined with sequence-based phylogenetic analysis, revealed a fundamental split among **bacteria.** DNA-dependent RNA polymerase subunits of Group I, which includes Proteobacteria, Aquifex, Chlamydia, Spirochaetes, Cytophaga-Chlorobium, and Planctomycetes, are characterized by three distinct **inserts**, namely a Sandwich Barrel Hybrid Motif domain in the beta subunit, a beta-beta' module (BBM) 1 domain in the beta' subunit, and a distinct helical module in the sigma subunit. The DdRp subunits of remaining bacteria, which comprise Group II, lack these **inserts**, although some additional **inserted** domains are present in individual lineages. The separation of bacteria into Group I and Group II is generally compatible with the topologies of phylogenetic trees of the conserved regions of DdRp subunits and concatenated ribosomal proteins and might represent the primary bifurcation in bacterial evolution. A striking deviation from this evolutionary pattern is Aquifex whose DdRp subunits cluster within Group I, whereas phylogenetic analysis of ribosomal proteins identifies Aquifex as grouping with Thermotoga another bacterial hyperthemophile belonging to Group II. The inferred evolutionary scenario for the DdRp subunits includes domain accretion and rearrangement, with some likely horizontal transfer events. Although evolution of bacterial DdRp appeared to be generally dominated by vertical inheritance, horizontal transfer of complete genes for all or some of the subunits, resulting in displacement of the ancestral genes, might have played a role in several lineages, such as Aquifex, Thermotoga, and

Fusobacterium.

L10 ANSWER 3 OF 2322 MEDLINE on STN
ACCESSION NUMBER: 2004255613 IN-PROCESS
DOCUMENT NUMBER: PubMed ID: 15133095
TITLE: Emergence of phenotypic variants upon mismatch repair disruption in Pseudomonas aeruginosa.
AUTHOR: Smania Andrea M; Segura Ignacio; Pezza Roberto J; Becerra Cecilia; Albesa Ines; Argarana Carlos E
CORPORATE SOURCE: Centro de Investigaciones en Quimica Biologica de Cordoba (CIQUIBIC), CONICET, Departamento de Quimica Biologica, Facultad de Ciencias Quimicas, Universidad Nacional de Cordoba, Ciudad Universitaria, 5000 Cordoba, Argentina.. asmania@dqb.fcq.unc.edu.ar
SOURCE: Microbiology (Reading, England), (2004 May) 150 (Pt 5) 1327-38.
Journal code: 9430468. ISSN: 1350-0872.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20040525
Last Updated on STN: 20040525

AB MutS is part of the **bacterial** mismatch repair system that corrects point mutations and small **insertions**/deletions that fail to be proof-read by DNA **polymerase** activity. In this work it is shown that the disruption of the P. aeruginosa mutS gene generates the emergence of diverse colony morphologies in contrast with its parental wild-type strain that displayed monomorphic colonies. Interestingly, two of the mutS morphotypes emerged at a high frequency and in a reproducible way and were selected for subsequent characterization. One of them displayed a nearly wild-type morphology while the other notably showed, compared with the wild-type strain, increased production of pyocyanin and pyoverdin, lower excretion of LasB protease and novel motility characteristics, mainly related to swarming. Furthermore, it was reproducibly observed that, after prolonged incubation in liquid culture, the pigmented variant consistently emerged from the mutS wild-type-like variant displaying a reproducible event. It is also shown that these P. aeruginosa mutS morphotypes not only displayed an increase in the frequency of antibiotic-resistant mutants, as described for clinical P. aeruginosa mutator isolates, but also generated mutants whose antibiotic-resistant levels were higher than those measured from spontaneous resistant mutants derived from wild-type cells. It was also found that both morphotypes showed a decreased cytotoxic capacity compared to the wild-type strain, leading to the emergence of invasive variants. By using mutated versions of a tetracycline resistance gene, the mutS mutant showed a 70-fold increase in the reversion frequency of a +1 frameshift mutation with respect to its parental wild-type strain, allowing the suggestion that the phenotypical diversity generated in the mutS population could be produced in part by frameshift mutations. Finally, since morphotypical diversification has also been described in clinical isolates, the possibility that this mutS diversification was related to the high frequency hypermutability observed in P. aeruginosa CF isolates is discussed.

L10 ANSWER 4 OF 2322 MEDLINE on STN
ACCESSION NUMBER: 2004216323 IN-PROCESS
DOCUMENT NUMBER: PubMed ID: 15114006
TITLE: Transient and inducible expression of vaccinia/t7 recombinant viruses.
AUTHOR: Mohamed Mohamed Ragaa; Niles Edward G
SOURCE: Methods in molecular biology (Clifton, N.J.), (2004) 269 41-50.
Journal code: 9214969. ISSN: 1064-3745.

PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-DATA-REVIEW; IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20040429
Last Updated on STN: 20040429

AB Recombinant DNA technology has made it possible to develop molecular cloning vectors that allow the expression of heterologous genes in a variety of animal viruses. This chapter discusses the use of vaccinia virus encoding **bacteriophage** T7 RNA **polymerase** as an expression vector system. A chosen gene is **inserted** into a plasmid vector designed to express genes under the control of the T7 promoter. Transient expression can then be achieved either by transfecting this plasmid into cells infected with the recombinant vaccinia virus expressing T7 RNA polymerase, vTF7-3 or by crossing this plasmid into the vaccinia virus genome and coinfecting cells with both viruses. Moreover, placement of lacO downstream of the vaccinia virus P11 late promoter regulating T7 RNA polymerase expression, and integration of lacI under vaccinia promoter control into the viral genome, vT7lacOI, yielded a recombinant virus capable of IPTG-inducible T7 promoter-controlled expression of foreign genes.

L10 ANSWER 5 OF 2322 MEDLINE on STN
ACCESSION NUMBER: 2004106967 MEDLINE
DOCUMENT NUMBER: PubMed ID: 14976253
TITLE: Blue light-induced transcription of plastid-encoded psbD gene is mediated by a nuclear-encoded transcription initiation factor, AtSig5.
AUTHOR: Tsunoyama Yuichi; Ishizaki Yoko; Morikawa Kazuya; Kobori Maki; Nakahira Yoichi; Takeba Go; Toyoshima Yoshinori; Shiina Takashi
CORPORATE SOURCE: Radioisotope Research Center, Kyoto University, Kitashirakawa-oiwake-cho, Sakyo-ku Kyoto 606-8502, Japan.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (2004 Mar 2) 101 (9) 3304-9. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200406
ENTRY DATE: Entered STN: 20040304
Last Updated on STN: 20040618
Entered Medline: 20040617

AB Light is one of the most important environmental factors regulating expression of photosynthesis genes. The plastid psbD gene encoding the photosystem II reaction center protein D2 is under the control of a unique blue light responsive promoter (BLRP) that is transcribed by a **bacterial**-type plastid RNA **polymerase** (PEP). Promoter recognition of PEP is mediated by one of the six nuclear-encoded sigma factors in Arabidopsis. The replacement of the plastid sigma factor associated with PEP may be the major mechanism for switching of plastid transcription pattern in response to environmental and developmental signals. This study demonstrates that AtSig5 is a unique sigma factor that is essential for psbD BLRP activity. A T-DNA **insertional** mutant with reduced AtSIG5 expression resulted in loss of primary transcripts from the psbD BLRP. Furthermore, transient overexpression of AtSig5 in dark-adapted protoplasts specifically elevated psbD and psbA transcription activities. On the other hand, overproduction of AtSig2 enhanced the transcription of psbA gene and trnE operon, but not psbD transcription. The AtSIG5 gene is phylogenetically distinct from other plastid sigma factors, and its expression is induced exclusively by blue light. We propose that AtSig5 acts as a mediator of blue light signaling that specifically activates the psbD BLRP in response to blue light in

Arabidopsis.

L10 ANSWER 6 OF 2322 MEDLINE on STN
ACCESSION NUMBER: 2004101058 MEDLINE
DOCUMENT NUMBER: PubMed ID: 14990691
TITLE: Presence of an encephalomyocarditis virus internal ribosome entry site sequence in avian infectious bronchitis virus defective RNAs abolishes rescue by helper virus.
AUTHOR: Dove Brian; Cavanagh David; Britton Paul
CORPORATE SOURCE: Division of Molecular Biology, Institute for Animal Health, Compton Laboratory, Compton, Newbury, Berkshire RG20 7NN, United Kingdom.
SOURCE: Journal of virology, (2004 Mar) 78 (6) 2711-21.
Journal code: 0113724. ISSN: 0022-538X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200404
ENTRY DATE: Entered STN: 20040302
Last Updated on STN: 20040409
Entered Medline: 20040408

AB Avian infectious bronchitis virus (IBV) defective RNAs (D-RNAs) have been used for the expression of heterologous genes in a helper-virus-dependent expression system. The heterologous genes were expressed under the control of an IBV transcription-associated sequence (TAS) derived from gene 5 of IBV Beaudette. However, coronavirus D-RNA expression vectors display an inherent instability following serial passage with helper virus, resulting in the eventual loss of the heterologous genes. The use of the picornavirus encephalomyocarditis virus (EMCV) internal ribosome entry site (IRES) sequence to initiate gene translation was investigated as an alternative method to the coronavirus-mediated TAS-controlled heterologous gene expression system. IBV D-RNAs containing the chloramphenicol acetyltransferase (CAT) reporter gene, under EMCV IRES control, were assessed for IRES-mediated CAT protein translation. CAT protein was detected from T7-derived IBV D-RNA transcripts in a cell-free protein synthesis system and in situ in avian chick kidney (CK) cells following T7-derived D-RNA synthesis from a recombinant fowlpox virus expressing the **bacteriophage** T7 DNA-dependent RNA **polymerase.** However, CAT protein was not detected in CK cells from IRES-containing IBV D-RNAs, in which the IRES-CAT construct was **inserted** at two different positions within the D-RNA, in the presence of helper IBV. Northern blot analysis demonstrated that the IRES-containing D-RNAs were not rescued on serial passage with helper virus, indicating that the EMCV IRES sequence had a detrimental effect on IBV D-RNA rescue.

L10 ANSWER 7 OF 2322 MEDLINE on STN
ACCESSION NUMBER: 2004020719 MEDLINE
DOCUMENT NUMBER: PubMed ID: 14717593
TITLE: Evaluating the contribution of base stacking during translesion DNA replication.
AUTHOR: Reineks Edmunds Z; Berdis Anthony J
CORPORATE SOURCE: Department of Pharmacology and the Comprehensive Cancer Center, School of Medicine, Case Western Reserve University, 10900 Euclid Avenue, Cleveland, Ohio 44106, USA.
SOURCE: Biochemistry, (2004 Jan 20) 43 (2) 393-404.
Journal code: 0370623. ISSN: 0006-2960.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200405

ENTRY DATE: Entered STN: 20040114
Last Updated on STN: 20040526
Entered Medline: 20040525

AB Despite the nontemplating nature of the abasic site, dAMP is often preferentially **inserted** opposite the lesion, a phenomenon commonly referred to as the "A-rule". We have evaluated the molecular mechanism accounting for this unique behavior using a thorough kinetic approach to evaluate polymerization efficiency during translesion DNA replication. Using the **bacteriophage** T4 DNA **polymerase**, we have measured the **insertion** of a series of modified nucleotides and have demonstrated that increasing the size of the nucleobase does not correlate with increased **insertion** efficiency opposite an abasic site. One analogue, 5-nitroindolyl-2'-deoxyriboside triphosphate, was unique as it was **inserted** opposite the lesion with approximately 1000-fold greater efficiency compared to that for dAMP **insertion.** Pre-steady-state kinetic measurements yield a kpol value of 126 s(-1) and a Kd value of 18 microM for the **insertion** of 5-nitroindolyl-2'-deoxyriboside triphosphate opposite the abasic site. These values rival those associated with the enzymatic formation of a natural Watson-Crick base pair. These results not only reiterate that hydrogen bonding is not necessary for nucleotide **insertion** but also indicate that the base-stacking and/or desolvation capabilities of the incoming nucleobase may indeed play the predominant role in generating efficient DNA polymerization. A model accounting for the increase in catalytic efficiency of this unique nucleobase is provided and invokes pi-pi stacking interactions of the aromatic moiety of the incoming nucleobase with aromatic amino acids present in the polymerase's active site. Finally, differences in the rate of 5-nitroindolyl-2'-deoxyriboside triphosphate **insertion** opposite an abasic site are measured between the **bacteriophage** T4 DNA **polymerase** and the Klenow fragment. These kinetic differences are interpreted with regard to the differences in various structural components between the two enzymes and are consistent with the proposed model for DNA polymerization.

L10 ANSWER 8 OF 2322 MEDLINE on STN
ACCESSION NUMBER: 2003604068 IN-PROCESS
DOCUMENT NUMBER: PubMed ID: 14686583
TITLE: CCLS96.1, a member of a multicopy gene family, may encode a non-coding RNA preferentially transcribed in reproductive organs of Silene latifolia.
AUTHOR: Sugiyama Ryuji; Kazama Yusuke; Miyazawa Yutaka; Matsunaga Sachihiro; Kawano Shigeyuki
CORPORATE SOURCE: Department of Biological Sciences, Graduate School of Science, University of Tokyo, 7-3-1 Hongo, Bunkyo, Tokyo 113-0033, Japan.. sugiyama@biol.s.u-tokyo.ac.jp
SOURCE: DNA research : an international journal for rapid publication of reports on genes and genomes, (2003 Oct 31) 10 (5) 213-20.
Journal code: 9423827. ISSN: 1340-2838.
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20031223
Last Updated on STN: 20031223

AB Dioecy in the model dioecious plant Silene latifolia is determined genetically by its heteromorphic sex chromosomes. A **bacterial** artificial chromosome (BAC) clone, #19B12, was isolated by screening a BAC library from S. latifolia using **polymerase** chain reaction (PCR) with a set of sequence tagged site (STS) primers, ScD05, which are specific to the Y chromosome. A portion of #19B12 was subcloned to construct plasmid #25-1, with an **insert** of 7.8 kb. This 7.8-kb fragment encodes ScD05 homolog and an anther-specific gene, CCLS96.1.

Northern blot analysis of CCLS96.1 indicated a faint band of 1.8 kb in male and female flower buds. 5' and 3' rapid amplification of cDNA ends (RACE) indicated that transcripts of CCLS96.1 are very varied in size. Moreover, semi-quantitative reverse transcription-PCR (RT-PCR) showed that CCLS96.1 was also expressed in both male and female leaves. RACE produced at least ten species of transcripts, with 79-97% similarity among them. However, no significant ORFs could be predicted from their nucleotide sequences, since each has numerous stop codons throughout all three reading frames. Genomic Southern hybridization showed that the S. latifolia genome contains numerous CCLS96.1 homologs. These results suggest that the transcripts of CCLS96.1 play some role as multiple non-coding RNAs in S. latifolia.

L10 ANSWER 9 OF 2322 MEDLINE on STN
ACCESSION NUMBER: 2003475131 MEDLINE
DOCUMENT NUMBER: PubMed ID: 14536071
TITLE: Separate **insertion** and deletion subcomplexes of the Trypanosoma brucei RNA editing complex.
AUTHOR: Schnaufer Achim; Ernst Nancy Lewis; Palazzo Setareh S; O'Rear Jeff; Salavati Reza; Stuart Kenneth
CORPORATE SOURCE: Seattle Biomedical Research Institute, 4 Nickerson Street, Suite 200, Seattle, WA 98109, USA.
CONTRACT NUMBER: AI14102 (NIAID)
SOURCE: Molecular cell, (2003 Aug) 12 (2) 307-19. Journal code: 9802571. ISSN: 1097-2765.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200311
ENTRY DATE: Entered STN: 20031011
Last Updated on STN: 20031219
Entered Medline: 20031125

AB The Trypanosoma brucei editosome catalyzes the maturation of mitochondrial mRNAs through the **insertion** and deletion of uridylates and contains at least 16 stably associated proteins. We examined physical and functional associations among these proteins using three different approaches: purification of complexes via tagged editing ligases TbREL1 and TbREL2, comprehensive yeast two-hybrid analysis, and coimmunoprecipitation of recombinant proteins. A purified TbREL1 subcomplex catalyzed precleaved deletion editing in vitro, while a purified TbREL2 subcomplex catalyzed precleaved **insertion** editing in vitro. The TbREL1 subcomplex contained three to four proteins, including a putative exonuclease, and appeared to be coordinated by the zinc finger protein TbMP63. The TbREL2 subcomplex had a different composition, contained the TbMP57 terminal uridylyl transferase, and appeared to be coordinated by the TbMP81 zinc finger protein. This study provides insight into the molecular architecture of the editosome and supports the existence of separate subcomplexes for deletion and **insertion** editing.

L10 ANSWER 10 OF 2322 MEDLINE on STN
ACCESSION NUMBER: 2003369671 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12903368
TITLE: Unnatural base pairs between 2-amino-6-(2-thienyl)purine and the complementary bases.
AUTHOR: Hirao I; Fujiwara T; Kimoto M; Mitsui T; Okuni T; Ohtsuki T; Yokoyama S
CORPORATE SOURCE: Yokoyama CytoLogic Project, ERATO, JST, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama 351-0198, Japan.
SOURCE: Nucleic acids symposium series, (2000) (44) 261-2. Journal code: 8007206. ISSN: 0261-3166.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200310
ENTRY DATE: Entered STN: 20030808
Last Updated on STN: 20031003
Entered Medline: 20031002

AB The unnatural base, 2-amino-6-(2-thienyl)purine (designated as s), instead of 2-amino-6-(N,N-dimethylamino)purine (designated as x), was designed in order to improve the specificity and efficiency of the base pairing with pyridin-2-one (designated as y). DNA fragments containing s were chemically synthesized, and the thermal stability and the enzymatic reactions involving the s-y pairing were examined. Thermal denaturation experiments showed that the DNA duplex (12-mer) containing the s-y pair was more stable than that containing the x-y pair. The incorporation of dyTP was also more advantageous to the s-y pairing than the x-y pairing in single-nucleotide **insertion** experiments using the Klenow fragment of Escherichia coli DNA polymerase I.

=> d his

(FILE 'HOME' ENTERED AT 11:57:47 ON 01 JUL 2004)

FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 11:57:54 ON 01 JUL 2004

L1 949985 S POLYMERASE?
L2 760 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (2N) L1
L3 2599 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1
L4 5927 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1) OR T3 OT T7 OR S
L5 32470 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) (S) L1) OR T3
L6 275 S L5 (S) INTRON?
L7 448 S L5 (2N) INTRON?
L8 131 DUP REM L6 (144 DUPLICATES REMOVED)
L9 74 S L8 AND PY<=1997
L10 2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT

=> s l5 and (intron (3n) (introduc? or non (2n) nativ?) or insert? or spliced)
L11 2322 L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT? OR SPLICED)

=> s l5 and (intron (3n))(introduc? or non (2n) nativ?) or insert? or spliced))
MISSING TERM '3A))(INTRODUC?'
The search profile that was entered contains a logical operator
followed immediately by a right parenthesis ')'.

=> s l5 and (intron (3n) ((introduc? or non (2n) nativ?) or insert? or spliced))
L12 37 L5 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSERT? OR SPLICED))

=> dup rem l12
PROCESSING COMPLETED FOR L12
L13 16 DUP REM L12 (21 DUPLICATES REMOVED)

=> s l13 and Py<=1997
2 FILES SEARCHED...
L14 11 L13 AND PY<=1997

=> d l14 ibib abs 1-14

L14 ANSWER 1 OF 11 MEDLINE on STN
ACCESSION NUMBER: 96152651 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8565067
TITLE: Beyond homing: competition between intron endonucleases confers a selective advantage on flanking genetic markers.

AUTHOR: Goodrich-Blair H; Shub D A
CORPORATE SOURCE: Department of Biological Sciences, State University of New York at Albany 12222, USA.
CONTRACT NUMBER: GM37746 (NIGMS)
SOURCE: Cell, **(1996 Jan 26)** 84 (2) 211-21.
Journal code: 0413066. ISSN: 0092-8674.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199603
ENTRY DATE: Entered STN: 19960315
Last Updated on STN: 19980206
Entered Medline: 19960301

AB The closely related B. subtilis **bacteriophages** SPO1 and SP82 have similar **introns inserted** into a conserved domain of their DNA **polymerase** genes. These introns encode endonucleases with unique properties. Other intron-encoded "homing" endonucleases cleave both strands of intronless DNA; subsequent repair results in unidirectional gene conversion to the intron-containing allele. In contrast, the enzymes described here cleave one strand on both intron-containing and intronless targets at different distances from their common **intron insertion** site. Most surprisingly, each enzyme prefers DNA of the heterologous phage. The SP82-encoded endonuclease is responsible for exclusion of the SPO1 intron and flanking genetic markers from the progeny of mixed infections, a novel selective advantage imparted by an intron to the genome in which it resides.

L14 ANSWER 2 OF 11 MEDLINE on STN
ACCESSION NUMBER: 96069407 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8524264
TITLE: Cotranscriptional splicing of a group I intron is facilitated by the Cbp2 protein.
AUTHOR: Lewin A S; Thomas J Jr; Tirupati H K
CORPORATE SOURCE: Department of Molecular Genetics and Microbiology, University of Florida College of Medicine, Gainesville 32610-0266, USA.
CONTRACT NUMBER: GM12228 (NIGMS)
SOURCE: Molecular and cellular biology, **(1995 Dec)** 15 (12) 6971-8.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199601
ENTRY DATE: Entered STN: 19960219
Last Updated on STN: 20030202
Entered Medline: 19960119

AB The nuclear CBP2 gene encodes a protein essential for the splicing of a mitochondrial group I intron in Saccharomyces cerevisiae. This **intron** (bI5) is **spliced** autocatalytically in the presence of high concentrations of magnesium and monovalent salt but requires the Cbp2 protein for splicing under physiological conditions. Addition of Cbp2 during RNA synthesis permitted cotranscriptional splicing. Splicing did not occur in the transcription buffer in the absence of synthesis. The Cbp2 protein appeared to modify the folding of the intron during RNA synthesis: pause sites for RNA polymerase were altered in the presence of the protein, and some mutant transcripts that did not splice after transcription did so during transcription in the presence of Cbp2. Cotranscriptional splicing also reduced hydrolysis at the 3' splice junction. These results suggest that Cbp2 modulates the sequential folding of the ribozyme during its synthesis. In addition, splicing during transcription led to an increase in RNA synthesis with

both T7 RNA polymerase and mitochondrial RNA polymerase, implying a functional coupling between transcription and splicing.

L14 ANSWER 3 OF 11 MEDLINE on STN
ACCESSION NUMBER: 91355869 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2103447
TITLE: Analysis of the genes encoding the largest subunit of RNA polymerase II in Arabidopsis and soybean.
AUTHOR: Dietrich M A; Prenger J P; Guilfoyle T J
CORPORATE SOURCE: Department of Plant Biology, University of Minnesota, St. Paul 55108.
CONTRACT NUMBER: 1 U41 RR-01685-05 (NCRR)
GM37950 (NIGMS)
SOURCE: Plant molecular biology, **(1990 Aug)** 15 (2) 207-23.
Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X52492; GENBANK-X52493; GENBANK-X52494; GENBANK-X52495
ENTRY MONTH: 199110
ENTRY DATE: Entered STN: 19911027
Last Updated on STN: 19970203
Entered Medline: 19911004

AB We have cloned and sequenced the gene encoding the largest subunit of RNA polymerase II (RPB1) from Arabidopsis thaliana and partially sequenced genes from soybean (Glycine max). We have also determined the nucleotide sequence for a number of cDNA clones which encode the carboxyl terminal domains (CTDs) of RNA polymerase II from both soybean and Arabidopsis. The Arabidopsis RPB1 gene encodes a polypeptide of approximately 205 kDa, consists of 12 exons, and encompasses more than 8 kb. Predicted amino acid sequence shows eight regions of similarity with the largest subunit of other **prokaryotic** and eukaryotic RNA **polymerases**, as well as a highly conserved CTD unique to RNA **polymerase** II. The CTDs in plants, like those in most other eukaryotes, consist of tandem heptapeptide repeats with the consensus amino acid sequence PTSPSYS. The portion of RPB1 which encodes the CTD in plants differs from that of RPB1 of animals and lower eukaryotes. All the plant genes examined contain 2-3 introns within the CTD encoding regions, and at least two plant genes contain an alternatively **spliced intron** in the 3' untranslated region. Several clustered amino acid substitutions in the CTD are conserved in the two plant species examined, but are not found in other eukaryotes. RPB1 is encoded by a multigene family in soybean, but a single gene encodes this subunit in Arabidopsis and most other eukaryotes.

L14 ANSWER 4 OF 11 MEDLINE on STN
ACCESSION NUMBER: 89039878 MEDLINE
DOCUMENT NUMBER: PubMed ID: 3185558
TITLE: Short donor site sequences **inserted** within the **intron** of beta-globin pre-mRNA serve for splicing in vitro.
AUTHOR: Mayeda A; Ohshima Y
CORPORATE SOURCE: Graduate School of Medical Sciences, University of Tsukuba, Ibaraki, Japan.
SOURCE: Molecular and cellular biology, **(1988 Oct)** 8 (10) 4484-91.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198812

ENTRY DATE: Entered STN: 19900308
Last Updated on STN: 19970203
Entered Medline: 19881221

AB We constructed **SP6**-human beta-globin derivative plasmids that included possible donor site (5' splice site) sequences at a specified position within the first intron. The runoff transcripts from these templates truncated in the second exon were examined for splicing in a nuclear extract from HeLa cells. In addition to the products from the authentic donor site, a corresponding set of novel products from the inserted, alternative donor site was generated. Thus, a short sequence **inserted** within an **intron** can be an active donor site signal in the presence of an authentic donor site. The active donor site sequences included a 9-nucleotide consensus sequence, 14- or 16-nucleotide sequences at the human beta-globin first or second donor, and those at simian virus 40 large T antigen or small t antigen donor. These included 3 to 8 nucleotides of an exon and 6 to 8 nucleotides of an intron. The activity of the inserted donor site relative to that of the authentic donor site depended on the donor sequence inserted. The relative activity also strongly depended on the concentrations of both KCl (40 to 100 mM) and MgCl2 (1.6 to 6.4 mM). At the higher KCl concentrations tested, all the inserted, or proximate, donor sites were more efficiently used. Under several conditions, some inserted donor sites were more active than was the authentic donor site. Our system provides an in vitro assay for donor site activity of a sequence to be tested.

L14 ANSWER 5 OF 11 MEDLINE on STN
ACCESSION NUMBER: 88291594 MEDLINE
DOCUMENT NUMBER: PubMed ID: 3331218
TITLE: Inhibition of in vitro splicing of a mouse insulin pre-mRNA by covalent cross-links in the intron region.
AUTHOR: Szeberenyi J; Wollenzien P L; Goldenberg C J
CORPORATE SOURCE: Department of Biology, University Medical School of Pecs, Hungary.
SOURCE: Acta biologica Hungarica, **(1987)** 38 (2) 267-77.
Journal code: 8404358. ISSN: 0236-5383.
PUB. COUNTRY: Hungary
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198808
ENTRY DATE: Entered STN: 19900308
Last Updated on STN: 19970203
Entered Medline: 19880829

AB Recent studies have indicated that in vitro splicing of a mouse insulin pre-mRNA by a HeLa cell nuclear extract is accompanied by the unwinding of substrate RNA. The present experiments were performed to determine whether this melting of the secondary structure of the precursor RNA is essential for the splicing reaction. 32P-labelled mouse insulin pre-mRNA synthesized in vitro in a **SP6** transcription system was cross-linked with aminomethyltrimethyl psoralen and fractionated by polyacrylamide gel electrophoresis. RNA species containing different intramolecular cross-links were eluted from the gel and the sites of cross-links were mapped by primer extension analysis using synthetic oligonucleotide primers. Under conditions that allow accurate in vitro splicing of intact pre-mRNA, precursor molecules with psoralen cross-links within their **intron** region were not **spliced** by a HeLa cell nuclear extract. This observation strongly supports the assumption that unwinding of precursor RNA molecules is necessary for the splicing reaction.

L14 ANSWER 6 OF 11 MEDLINE on STN
ACCESSION NUMBER: 87080257 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2431897
TITLE: Accurate in vitro splicing of two pre-mRNA plant introns in

a HeLa cell nuclear extract.
AUTHOR: Brown J W; Feix G; Frendewey D
SOURCE: EMBO journal, **(1986 Nov)** 5 (11) 2749-58.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198702
ENTRY DATE: Entered STN: 19900302
Last Updated on STN: 19970203
Entered Medline: 19870217

AB Two plant introns along with flanking exon sequences have been isolated from an amylase gene of wheat and a legumin gene of pea and cloned behind the phage **SP6** promoter. Pre-mRNAs produced by in vitro transcription with **SP6** RNA polymerase were tested for their ability to be spliced in a HeLa cell nuclear extract. The plant **introns** were accurately **spliced** and the predicted splice junctions were used. Lariat RNAs were observed as both intermediates and final products during the splicing reaction. The branch points were mapped to adenosine residues lying within sequences that showed good homology to the animal branch point consensus. Consensus sequences for the 5' and 3' splice junctions and for putative branch point sequences of plants were derived from an analysis of 168 plant intron sequences.

L14 ANSWER 7 OF 11 MEDLINE on STN
ACCESSION NUMBER: 86232612 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2940512
TITLE: Assembly in an in vitro splicing reaction of a mouse insulin messenger RNA precursor into a 60-40S ribonucleoprotein complex.
AUTHOR: Kaltwasser G; Spitzer S G; Goldenberg C J
CONTRACT NUMBER: AI-19370 (NIAID)
SOURCE: Nucleic acids research, **(1986 May 12)** 14 (9) 3687-701.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198607
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 19970203
Entered Medline: 19860703

AB An **SP6**/mouse insulin RNA precursor containing two exons and one **intron** can be **spliced** in a partially purified nuclear extract isolated from MOPC-315 mouse myeloma cells. We have detected the putative RNA splicing intermediate (intron-3'exon) in a lariat form, the excised intron in a lariat form, and the mRNA spliced product. The in vitro splicing reaction of gel-purified RNA precursors requires ATP and Mg2+ and was accompanied by the formation of a 60-40S ribonucleoprotein complex. The formation of the 60S complex requires ATP. At least two Sm snRNPs containing U1 and U2 RNAs are components of the 60-40S complex. The assemble of those snRNPs occurs early during the splicing reaction and it requires ATP and intron containing pre-mRNAs.

L14 ANSWER 8 OF 11 EMBASE
on STN
ACCESSION NUMBER: 96209464 EMBASE
DOCUMENT NUMBER: 1996209464
TITLE: Splicing of a group II intron in a functional transfer gene of Lactococcus lactis.
AUTHOR: Shearman C.; Godon J.-J.; Gasson M.
CORPORATE SOURCE: Institute of Food Research, Norwich Research Park,Colney,

Norwich NR4 7UA, United Kingdom
SOURCE: Molecular Microbiology, (1996) 21/1 (45-53).
ISSN: 0950-382X CODEN: MOMIEE
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB A chromosomally located sex factor that controls conjugation in Lactococcus lactis 712 has been cloned and sequenced, leading to the discovery of an open reading frame with homology to the maturases of group II self-splicing introns. Reverse transcriptase **polymerase** chain reaction amplification was used to demonstrate that the **intron** was **spliced** out of mRNA in vivo, and sequence analysis revealed the site of splicing. The **intron** was **inserted** within a sex-factor gene which encodes a protein with homology to proteins involved in rolling-circle DNA replication. Gene-disruption experiments were used to demonstrate that this mobA gene was essential for sex-factor transfer and this suggests that intron splicing is a necessary part of the conjugation process. The sequence of the intron was modelled to produce a secondary structure that exhibited several features characteristic of the IIA subgroup. Here we report the characterization of a new group II intron in the Gram-positive **bacterium** L. lactis and demonstrate for the first time in **bacteria** both splicing in vivo and an active role for the gene carrying the intron.

L14 ANSWER 9 OF 11 EMBASE
on STN
ACCESSION NUMBER: 92022310 EMBASE
DOCUMENT NUMBER: 1992022310
TITLE: Identification of a novel latency-specific splice donor signal within the herpes simplex virus type 1 2.0-kilobase latency-associated transcript (LAT): translation inhibition of LAT open reading frames by the intron within the 2.0-kilobase LAT.
AUTHOR: Spivack J.G.; Woods G.M.; Fraser N.W.
CORPORATE SOURCE: The Wistar Institute, 36th Street at Spruce,Philadelphia, PA 19104, United States
SOURCE: Journal of Virology, (1991) 65/12 (6800-6810).
ISSN: 0022-538X CODEN: JOVIAM
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Herpes simplex virus type 1 establishes latent infection in trigeminal ganglia of mice infected via the eye. A family of three collinear viral transcripts (LATs), 2.0, 1.5, and 1.45 kb, is present in latently infected ganglia. To characterize these LATs, λgt10 cDNA libraries were constructed with RNAs isolated from the trigeminal ganglia of latently infected mice. A series of recombinant **bacteriophage** were isolated containing cDNA inserts covering 1.7 kb of the 2.0-kb LAT. Splice junctions of the smaller LATs and the 3' end of the 2.0-kb LAT were identified by sequence analysis of RNA **polymerase** chain reaction products. No splice was detected in the 2.0-kb LAT. The 3' end of the 2.0-kb LAT in vivo is upstream of a consensus splice acceptor site, which does not support the hypotheses that the 2.0-kb LAT is an intron. However, the data are consistent with the possibility of a short leader sequence or multiple LAT transcription start sites. To generate the smaller 1.5- and 1.45-kb LATs, there is a 559-nucleotide **intron spliced** from the 2.0-kb LAT in strain F and a 556-nucleotide intron in strain 17+. The nucleotide sequences at the 5' and 3' ends of these **introns** are characteristic of **spliced** transcripts from eukaryotic protein-encoding genes, with one significant difference; i.e., the 5' end

of the LAT intron is GC instead of the consensus sequence GT. This splice donor sequence is conserved in herpes simplex virus type 1 strains F, 17+, and KOS. Processing of the 2.0-kb LAT to form the spliced LATs preserves two open reading frames (ORFs) at the 3' end of the LATs; no new ORFs are created. Splicing of the LATs positions a 276-nucleotide leader sequence close to these ORFs and removes an intron that inhibits their translation in vitro. The novel 5' structure of the intron within the 2.0-kb LAT may be part of a control mechanism for transcription processing that results in splicing of the LATs only in sensory neurons during latent infection and reactivation but not during the viral replication cycle.

L14 ANSWER 10 OF 11 CA COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 127:322794 CA
TITLE: Property-affecting and/or property-exhibiting compositions for therapeutic and diagnostic uses
INVENTOR(S): Rabbani, Elazar; Stavrianopoulos, Jannis G.; Donegan, James J.; Liu, Dakai; Kelker, Norman E.; Engelhardt, Dean L.
PATENT ASSIGNEE(S): Enzo Therapeutics, Inc., USA
SOURCE: Can. Pat. Appl., 275 pp.
CODEN: CPXXEB
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
CA 2190304	AA	19970616	CA 1996-2190304	19961114 <--
EP 779365	A2	19970618	EP 1996-119961	19961212 <--
EP 779365	A3	19991124		
R: DE, FR, GB, IT				
JP 09313190	A2	19971209	JP 1996-360043	19961216 <--
US 2001006814	A1	20010705	US 1997-978633	19971125
US 2001006815	A1	20010705	US 1997-978634	19971125
US 2001006816	A1	20010705	US 1997-978637	19971125
US 2001007767	A1	20010712	US 1997-978632	19971125
US 2003087434	A1	20030508	US 1997-978635	19971125
US 2003104620	A1	20030605	US 1997-978636	19971125

PRIORITY APPLN. INFO.: US 1995-574443 A 19951215

AB Compns. useful for effecting and/or exhibiting changes in biol. functioning and processing in cells and biol. systems are provided which combine chemical modifications and/or ligand addns. with biol. functions in such a way as not to interfere substantially with the biol. functions. Such addnl. characteristics include nuclease resistance, targeting specific cells or cell receptors, and augmenting or decreasing interactions between the compns. and target cells. A title composition may constitute a nucleotide, nucleotide analog, nucleic acid, natural or synthetic polymer, ligand, or conjugate of a ligand with any of the preceding. For example, single-stranded DNA from a plasmid containing a gene of interest is complexed with an allylamine phosphoramidite-containing oligonucleotide primer (complementary to a region of the DNA distant from the gene of interest) which as been modified with trilactosyllysyllysine (preparation given), and the primer is extended with Klenow enzyme to form completely double-stranded DNA. On exposure of target cells to this DNA, the galactose moieties on the DNA bind to receptors on the cells, resulting in transport of the DNA into the cells. In another embodiment, DNA for antisense RNA sequences to regions of the HIV genome were inserted into the U1 small nuclear RNA coding region and the DNA was used to transform U937 cells. The transformed cells were resistant to HIV infection, as shown by inhibition of virus replication and p24 antigen production

L14 ANSWER 11 OF 11 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN

ACCESSION NUMBER: 95:570259 SCISEARCH
THE GENUINE ARTICLE: BD51W
TITLE: RECOMBINATION APPARATUS OF T4 PHAGE
AUTHOR: YONESAKI T (Reprint)
CORPORATE SOURCE: OSAKA UNIV, FAC SCI, DEPT BIOL, TOYONAKA, OSAKA 560, JAPAN (Reprint); OSAKA UNIV, COLL GEN EDUC, DEPT BIOL, TOYONAKA, OSAKA 560, JAPAN
COUNTRY OF AUTHOR: JAPAN
SOURCE: ADVANCES IN BIOPHYSICS, (**1995**) Vol. 31, pp. 3-22

ISSN: 0065-227X.
DOCUMENT TYPE: General Review; Journal
LANGUAGE: ENGLISH
REFERENCE COUNT: 95

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB T4 is a large **bacteriophage** carrying a linear 171-kb long double-stranded DNA (dsDNA) as its genome. Since the mature DNA molecules are cut with a 3% terminal redundancy from concatenated precursors, the genome contains a unique 166-kb sequence. Conventional genetic analysis has led to the discovery of about 120 genes on the genome, and ongoing sequencing of the T4 DNA has added more than 170 unidentified open reading frames (1-3). The large number of genes and open reading frames would imply that the T4 metabolism required for its propagation is much less dependent on host genes than that of other small phages. Except for the host genes for RNA **polymerase**, which enzyme primes viral DNA synthesis at origins, the Escherichia coli genes so far studied have been shown to have no effects on T4 DNA replication and genetic recombination in normal T4 infection. Thus, T4 genes seem to encode almost all of the proteins required for T4's own DNA replication or genetic recombination. The extensive genetic analyses conducted thus far have successfully identified many of the T4 genes involved in DNA metabolism, and in vitro studies of reactions catalyzed by the purified T4 gene products have taught us a great deal about the molecular mechanism of DNA metabolism.

DNA recombination is a multistep reaction in which a certain set of proteins is involved. Three different types of recombination are reported to occur in the T4 system. Two of them take place in limited regions of the T4 DNA. One is the reaction generating recombination hot spots. This reaction absolutely depends on the DNA replication origins and does not require DNA synaptases, T4 uvsX protein and E. coli recA protein, which are essential for general recombination (4). The other involves site-specific transposition of introns (intron homing) by a gene-conversion-like mechanism. A unique endonuclease encoded by a gene within T4 **introns introduces** a site-specific double-strand break to initiate the reaction (5, 6). A double-strand gap is subsequently generated by both 5' -> 3' and 3' -> 5' exonucleases. Protruding single-stranded DNAs (ssDNAs) flanking the gap are then utilized for strand transfer by DNA synaptase (7). Little of the precise mechanism and genes involved is known in these recombination reactions, since genetic analysis of the two types of recombination has only lately been begun. The third reaction is the well-characterized general recombination that can take place all over the T4 genomic DNA whenever a sequence homology exists. Extensive genetic analyses for more than 20 years and biochemical analyses over the past 10 years have allowed us to gain some insight into this reaction. Here, I will merely focus on general recombination and summarize the properties of the known proteins as well as genes involved in the reaction.

=> d his

(FILE 'HOME' ENTERED AT 11:57:47 ON 01 JUL 2004)

FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 11:57:54 ON 01 JUL 2004

```
L1       949985 S POLYMERASE?
L2          760 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (2N) L1
L3         2599 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1
L4         5927 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1) OR T3 OT T7 OR S
L5        32470 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) (S) L1) OR T3
L6          275 S L5 (S) INTRON?
L7          448 S L5 (2N) INTRON?
L8          131 DUP REM L6 (144 DUPLICATES REMOVED)
L9           74 S L8 AND PY<=1997
L10        2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L11        2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L12          37 S L5 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSER
L13          16 DUP REM L12 (21 DUPLICATES REMOVED)
L14          11 S L13 AND PY<=1997

=> s l1 and (intron (3n) ((introduc? or non (2n) nativ?) or insert? or spliced or))
MISSING TERM 'OR))'
The search profile that was entered contains a logical operator
followed immediately by a right parenthesis ')'.

=> s l1 and (intron (3n) ((introduc? or non (2n) nativ?) or insert? or spliced))
L15        1023 L1 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSERT?
                OR SPLICED))

=> s l15 and ((non (n) eu!aryot?) or pro!aryot? or bacter?) or T3 ot T7 or SP6
L16        3471 L15 AND ((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3 OT
                T7 OR SP6

=> s l15 and (((non (n) eu!aryot?) or pro!aryot? or bacter?) or T3 ot T7 or SP6)
L17         107 L15 AND (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
                OT T7 OR SP6)

=> s l15 (p) (((non (n) eu!aryot?) or pro!aryot? or bacter?) or T3 ot T7 or SP6)
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L85 (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L86 (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L87 (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L88 (P) '
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L89 (P) '
L18         107 L15 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
                OT T7 OR SP6)

=> s l17 and (l1 (p) (((non (n) eu!aryot?) or pro!aryot? or bacter?) or T3 ot T7 or
SP6))
L19          46 L17 AND (L1 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?)
                OR T3 OT T7 OR SP6))

=> s l17 and (l1 (s) (((non (n) eu!aryot?) or pro!aryot? or bacter?) or T3 ot T7 or
SP6))
L20          28 L17 AND (L1 (S) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?)
                OR T3 OT T7 OR SP6))

=> dup rem l20
PROCESSING COMPLETED FOR L20
L21          12 DUP REM L20 (16 DUPLICATES REMOVED)

=> d his

     (FILE 'HOME' ENTERED AT 11:57:47 ON 01 JUL 2004)
```

```
      FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 11:57:54 ON 01
      JUL 2004
L1        949985 S POLYMERASE?
L2           760 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (2N) L1
L3          2599 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1
L4          5927 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1) OR T3 OT T7 OR S
L5         32470 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) (S) L1) OR T3
L6           275 S L5 (S) INTRON?
L7           448 S L5 (2N) INTRON?
L8           131 DUP REM L6 (144 DUPLICATES REMOVED)
L9            74 S L8 AND PY<=1997
L10         2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L11         2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L12           37 S L5 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSER
L13           16 DUP REM L12 (21 DUPLICATES REMOVED)
L14           11 S L13 AND PY<=1997
L15         1023 S L1 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSERT
L16         3471 S L15 AND ((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L17          107 S L15 AND (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L18          107 S L15 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L19           46 S L17 AND (L1 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTE
L20           28 S L17 AND (L1 (S) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTE
L21           12 DUP REM L20 (16 DUPLICATES REMOVED)

=> s l21 not l14
L22            5 L21 NOT L14

=> s l22 and py<=1995
   2 FILES SEARCHED...
L23            0 L22 AND PY<=1995

=> d his

      (FILE 'HOME' ENTERED AT 11:57:47 ON 01 JUL 2004)

      FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 11:57:54 ON 01
      JUL 2004
L1        949985 S POLYMERASE?
L2           760 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (2N) L1
L3          2599 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1
L4          5927 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1) OR T3 OT T7 OR S
L5         32470 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) (S) L1) OR T3
L6           275 S L5 (S) INTRON?
L7           448 S L5 (2N) INTRON?
L8           131 DUP REM L6 (144 DUPLICATES REMOVED)
L9            74 S L8 AND PY<=1997
L10         2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L11         2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L12           37 S L5 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSER
L13           16 DUP REM L12 (21 DUPLICATES REMOVED)
L14           11 S L13 AND PY<=1997
L15         1023 S L1 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSERT
L16         3471 S L15 AND ((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L17          107 S L15 AND (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L18          107 S L15 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L19           46 S L17 AND (L1 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTE
L20           28 S L17 AND (L1 (S) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTE
L21           12 DUP REM L20 (16 DUPLICATES REMOVED)
L22            5 S L21 NOT L14
L23            0 S L22 AND PY<=1995

=> d l22 ibib abs 1-5

L22  ANSWER 1 OF 5     MEDLINE on STN
```

ACCESSION NUMBER: 1999045290 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9829825
TITLE: Characterization of a gene encoding a single-subunit **bacteriophage**-type RNA **polymerase** from maize which is alternatively spliced.
AUTHOR: Young D A; Allen R L; Harvey A J; Lonsdale D M
CORPORATE SOURCE: Department of Molecular Genetics, John Innes Centre, Colney, Norwich, UK.
SOURCE: Molecular & general genetics : MGG, (1998 Oct) 260 (1) 30-7.
Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AJ005343; GENBANK-AJ005344
ENTRY MONTH: 199812
ENTRY DATE: Entered STN: 19990115
Last Updated on STN: 19990115
Entered Medline: 19981207

AB Single-subunit RNA **polymerases** belonging to the T3/T7 **bacteriophage** family are thought to be common throughout eukaryotes. We report the isolation and characterization of a nucleus-encoded single-subunit RNA **polymerase** gene from maize. This gene is highly homologous to other single-subunit RNA **polymerase** genes from Arabidopsis, Chenopodium. yeast and Neurospora crassa involved in organellar transcription. Genomic Southern analysis reveals 10 to 15 hybridising fragments, suggesting that maize contains a small gene family. The isolated gene contains 19 exons and its genomic structure is highly conserved when compared to the three Arabidopsis homologues. Unlike the case in Arabidopsis, intron-12 of the maize **bacteriophage**-type RNA **polymerase** gene is alternatively spliced. Quantitative RT-PCR revealed that the resultant alternatively spliced transcript represents approximately 21 to 26% of the total **polymerase** mRNA in maize coleoptiles. The orthologous wheat **bacteriophage**-type RNA **polymerase** is also alternatively **spliced** and the **intron** exhibits 78% identity to maize intron-12. The conservation in alternative splicing between wheat and maize and its absence from Arabidopsis suggest a functional requirement for the alternatively spliced product.

L22 ANSWER 2 OF 5 EMBASE
on STN
ACCESSION NUMBER: 2003382831 EMBASE
TITLE: A group II intron has invaded the genus Azotobacter and is inserted within the termination codon of the essential groEL gene.
AUTHOR: Ferat J.-L.; Le Gouar M.; Michel F.
CORPORATE SOURCE: J.-L. Ferat, Ctr. de Genet. Molec. du CNRS, 91190 Gifsur-Yvette, France. ferat@cgm.cnr-gif.fr
SOURCE: Molecular Microbiology, (2003) 49/5 (1407-1423).
Refs: 64
ISSN: 0950-382X CODEN: MOMIEE
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB A group II intron that was previously identified within Azotobacter vinelandii by **polymerase** chain reaction with consensus primers has been completely sequenced, together with its flanking exons. In contrast to other **bacterial** members of group II, which are associated with mobile or other presumably non-essential DNA, the A. vinelandii **intron** is **inserted** within the termination

codon of the groEL coding sequence, which it changes from UAA to UAG. Both the host gene and the intron appear to be functional as (i) the ribozyme component of the intron self-splices in vitro and (ii) both intron-carrying and intronless versions of the single-copy groEL gene from A. vinelandii complement groEL mutations in Escherichia coli. Moreover, analysis of nucleotide substitutions within and around a closely related intron sequence that is present at the same site in Azotobacter chroococcum provides indirect evidence of intron transposition posterior to the divergence of the two Azotobacter taxa. Somewhat surprisingly, however, analyses of RNA extracted from cells that had or had not undergone a heat shock show that the bulk of groEL transcripts end within the first 140 nucleotides of the intron. These findings are discussed in the light of our current knowledge of the biochemistry of group II introns.

L22 ANSWER 3 OF 5 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 2002183703 EMBASE
TITLE: Two self-splicing group I introns in the ribonucleotide reductase large subunit gene of Staphylococcus aureus phage Twort.
AUTHOR: Landthaler M.; Begley U.; Lau N.C.; Shub D.A.
CORPORATE SOURCE: D.A. Shub, Dept. of Biol. Sci./Ctr. Mol. Genet., University at Albany, State University of New York, 1400 Washington Avenue, Albany, NY 12222, United States. shub@albany.edu
SOURCE: Nucleic Acids Research, (1 May 2002) 30/9 (1935-1943). Refs: 40
ISSN: 0305-1048 CODEN: NARHAD
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We have recently described three group I **introns** **inserted** into a single gene, orf142, of the staphylococcal **bacteriophage** Twort and suggested the presence of at least two additional self-splicing introns in this phage genome. Here we report that two previously uncharacterized introns, 429 and 1087 nt in length, interrupt the Twort gene coding for the large subunit of ribonucleotide reductase (nrdE). Reverse transcription-**polymerase** chain reaction (RT-PCR) of RNA isolated from Staphylococcus aureus after phage infection indicates that the introns are removed from the primary transcript in vivo. Both nrdE introns show sequence similarity to the Twort orf142 introns 12 and 13, suggesting either a common origin of these introns or shuffling of intron structural elements. Intron 2 encodes a DNA endonuclease, I-TwoI, with similarity to homing endonucleases of the HNH family. Like I-HmuI and I-HmuII, intron-encoded HNH endonucleases in Bacillus subtilis phages SPO1 and SP82, I-TwoI nicks only one strand of its DNA recognition sequence. However, whereas I-HmuI and I-HmuII cleave the template strand in exon 2, I-TwoI cleaves the coding strand in exon 1. In each case, the 3' OH created on the cut strand is positioned to prime DNA synthesis towards the intron, suggesting that this reaction contributes to the mechanism of intron homing. Both nrdE **introns** are **inserted** in highly conserved regions of the ribonucleotide reductase gene, next to codons for functionally important residues.

L22 ANSWER 4 OF 5 CA COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 139:241054 CA
TITLE: The nicking homing endonuclease I-BasI is encoded by a group I intron in the DNA **polymerase** gene of the Bacillus thuringiensis phage Bastille
AUTHOR(S): Landthaler, Markus; Shub, David A.
CORPORATE SOURCE: Department of Biological Sciences and Center for Molecular Genetics, University at Albany, SUNY,

Albany, NY, USA
SOURCE: Nucleic Acids Research (2003), 31(12), 3071-3077
CODEN: NARHAD; ISSN: 0305-1048
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Here we describe the discovery of a group I intron in the DNA **polymerase** gene of Bacillus thuringiensis phage Bastille. Although the **intron insertion** site is identical to that of the Bacillus subtilis phages SPO1 and SP82 introns, the Bastille intron differs from them substantially in primary and secondary structure. Like the SPO1 and SP82 introns, the Bastille intron encodes a nicking DNA endonuclease of the H-N-H family, I-BasI, with a cleavage site identical to that of the SPO1-encoded enzyme I-HmuI. Unlike I-HmuI, which nicks both intron-minus and intron-plus DNA, I-BasI cleaves only intron-minus alleles, which is a characteristic of typical homing endonucleases. Interestingly, the C-terminal portions of these H-N-H phage endonucleases contain a conserved sequence motif, the intron-encoded endonuclease repeat motif (IENR1) that also has been found in endonucleases of the GIY-YIG family, and which likely comprises a small DNA-binding module with a globular ββααβ fold, suggestive of module shuffling between different homing endonuclease families.
REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L22 ANSWER 5 OF 5 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 2003:570633 SCISEARCH
THE GENUINE ARTICLE: 697TU
TITLE: Molecular characterization of lysozyme type II gene in rainbow trout (Oncorhynchus mykiss): Evidence of gene duplication
AUTHOR: Mitra A; Foster-Frey J; Rexroad C E; Wells K D; Wall R J (Reprint)
CORPORATE SOURCE: USDA ARS, Gene Evaluat & Mapping Lab, Beltsville, MD 20705 USA (Reprint); USDA ARS, Natl Ctr Cool & Cold Aquaculture, Lee Town, WV USA
COUNTRY OF AUTHOR: USA
SOURCE: ANIMAL BIOTECHNOLOGY, (JUL 2003) Vol. 14, No. 1, pp. 7-12. Publisher: MARCEL DEKKER INC, 270 MADISON AVE, NEW YORK, NY 10016 USA.
ISSN: 1049-5398.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 18
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Rainbow trout (Oncorhynchus mykiss) have two types of lysozyme. Type II lysozyme differs from type I by only one amino acid, but only type II lysozyme has significant **bactericidal** activity. Due to this novel antibacterial property, lysozyme type II appears to be a candidate gene for enhancing disease resistance in fish as well as livestock species. Using **polymerase** chain reaction the lysozyme type II gene was amplified from genomic DNA isolated from rainbow trout. Two amplified fragments of 2041 and 2589 bp were observed. Sequencing revealed both amplicons were lysozyme genes having nearly identical nucleotide sequences, except the longer fragment has 548 base pairs **inserted** in **intron** 2 at nucleotide position 513 and a few point mutations within intron 2. Both versions of trout lysozyme type II gene were comprised of four exons and three introns. We also demonstrated that trout lysozyme is most likely encoded by these two different genes.

=> d his

(FILE 'HOME' ENTERED AT 11:57:47 ON 01 JUL 2004)

```
      FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 11:57:54 ON 01
      JUL 2004
L1        949985 S POLYMERASE?
L2           760 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (2N) L1
L3          2599 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1
L4          5927 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1) OR T3 OT T7 OR S
L5         32470 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) (S) L1) OR T3
L6           275 S L5 (S) INTRON?
L7           448 S L5 (2N) INTRON?
L8           131 DUP REM L6 (144 DUPLICATES REMOVED)
L9            74 S L8 AND PY<=1997
L10         2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L11         2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L12           37 S L5 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSER
L13           16 DUP REM L12 (21 DUPLICATES REMOVED)
L14           11 S L13 AND PY<=1997
L15         1023 S L1 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSERT
L16         3471 S L15 AND ((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L17          107 S L15 AND (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L18          107 S L15 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L19           46 S L17 AND (L1 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTE
L20           28 S L17 AND (L1 (S) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTE
L21           12 DUP REM L20 (16 DUPLICATES REMOVED)
L22            5 S L21 NOT L14
L23            0 S L22 AND PY<=1995

=> s l19 and py=<1995
   2 FILES SEARCHED...
L24           13 L19 AND PY=<1995

=> s l24 not l22
L25           13 L24 NOT L22

=> dup rem l25
PROCESSING COMPLETED FOR L25
L26            5 DUP REM L25 (8 DUPLICATES REMOVED)

=> s l26 or l22
L27           10 L26 OR L22

=> dup rem l27
PROCESSING COMPLETED FOR L27
L28           10 DUP REM L27 (0 DUPLICATES REMOVED)

=> d l26 ibib abs 1-5

L26  ANSWER 1 OF 5     MEDLINE on STN
ACCESSION NUMBER:    96069407     MEDLINE
DOCUMENT NUMBER:     PubMed ID: 8524264
TITLE:               Cotranscriptional splicing of a group I intron is
                     facilitated by the Cbp2 protein.
AUTHOR:              Lewin A S; Thomas J Jr; Tirupati H K
CORPORATE SOURCE:    Department of Molecular Genetics and Microbiology,
                     University of Florida College of Medicine, Gainesville
                     32610-0266, USA.
CONTRACT NUMBER:     GM12228 (NIGMS)
SOURCE:              Molecular and cellular biology, (1995 Dec) 15
                     (12) 6971-8.
                     Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY:        United States
DOCUMENT TYPE:       Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
```

ENTRY MONTH: 199601
ENTRY DATE: Entered STN: 19960219
Last Updated on STN: 20030202
Entered Medline: 19960119

AB The nuclear CBP2 gene encodes a protein essential for the splicing of a mitochondrial group I intron in Saccharomyces cerevisiae. This **intron** (bI5) is **spliced** autocatalytically in the presence of high concentrations of magnesium and monovalent salt but requires the Cbp2 protein for splicing under physiological conditions. Addition of Cbp2 during RNA synthesis permitted cotranscriptional splicing. Splicing did not occur in the transcription buffer in the absence of synthesis. The Cbp2 protein appeared to modify the folding of the intron during RNA synthesis: pause sites for RNA **polymerase** were altered in the presence of the protein, and some mutant transcripts that did not splice after transcription did so during transcription in the presence of Cbp2. Cotranscriptional splicing also reduced hydrolysis at the 3' splice junction. These results suggest that Cbp2 modulates the sequential folding of the ribozyme during its synthesis. In addition, splicing during transcription led to an increase in RNA synthesis with both T7 RNA **polymerase** and mitochondrial RNA **polymerase** , implying a functional coupling between transcription and splicing.

L26 ANSWER 2 OF 5 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 95:570259 SCISEARCH
THE GENUINE ARTICLE: BD51W
TITLE: RECOMBINATION APPARATUS OF T4 PHAGE
AUTHOR: YONESAKI T (Reprint)
CORPORATE SOURCE: OSAKA UNIV, FAC SCI, DEPT BIOL, TOYONAKA, OSAKA 560, JAPAN (Reprint); OSAKA UNIV, COLL GEN EDUC, DEPT BIOL, TOYONAKA, OSAKA 560, JAPAN
COUNTRY OF AUTHOR: JAPAN
SOURCE: ADVANCES IN BIOPHYSICS, (**1995**) Vol. 31, pp. 3-22

ISSN: 0065-227X.
DOCUMENT TYPE: General Review; Journal
LANGUAGE: ENGLISH
REFERENCE COUNT: 95

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB T4 is a large **bacteriophage** carrying a linear 171-kb long double-stranded DNA (dsDNA) as its genome. Since the mature DNA molecules are cut with a 3% terminal redundancy from concatenated precursors, the genome contains a unique 166-kb sequence. Conventional genetic analysis has led to the discovery of about 120 genes on the genome, and ongoing sequencing of the T4 DNA has added more than 170 unidentified open reading frames (1-3). The large number of genes and open reading frames would imply that the T4 metabolism required for its propagation is much less dependent on host genes than that of other small phages. Except for the host genes for RNA **polymerase**, which enzyme primes viral DNA synthesis at origins, the Escherichia coli genes so far studied have been shown to have no effects on T4 DNA replication and genetic recombination in normal T4 infection. Thus, T4 genes seem to encode almost all of the proteins required for T4's own DNA replication or genetic recombination. The extensive genetic analyses conducted thus far have successfully identified many of the T4 genes involved in DNA metabolism, and in vitro studies of reactions catalyzed by the purified T4 gene products have taught us a great deal about the molecular mechanism of DNA metabolism.

DNA recombination is a multistep reaction in which a certain set of proteins is involved. Three different types of recombination are reported to occur in the T4 system. Two of them take place in limited regions of the T4 DNA. One is the reaction generating recombination hot spots. This reaction absolutely depends on the DNA replication origins and does not require DNA synaptases, T4 uvsX protein and E. coli recA protein, which are essential for general recombination (4). The other involves site-specific transposition of introns (intron homing) by a

gene-conversion-like mechanism. A unique endonuclease encoded by a gene within T4 **introns introduces** a site-specific double-strand break to initiate the reaction (5, 6). A double-strand gap is subsequently generated by both 5' -> 3' and 3' -> 5' exonucleases. Protruding single-stranded DNAs (ssDNAs) flanking the gap are then utilized for strand transfer by DNA synaptase (7). Little of the precise mechanism and genes involved is known in these recombination reactions, since genetic analysis of the two types of recombination has only lately been begun. The third reaction is the well-characterized general recombination that can take place all over the T4 genomic DNA whenever a sequence homology exists. Extensive genetic analyses for more than 20 years and biochemical analyses over the past 10 years have allowed us to gain some insight into this reaction. Here, I will merely focus on general recombination and summarize the properties of the known proteins as well as genes involved in the reaction.

L26 ANSWER 3 OF 5 MEDLINE on STN DUPLICATE 1

ACCESSION NUMBER: 92046343 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1658375
TITLE: Identification of a novel latency-specific splice donor signal within the herpes simplex virus type 1 2.0-kilobase latency-associated transcript (LAT): translation inhibition of LAT open reading frames by the intron within the 2.0-kilobase LAT.
AUTHOR: Spivack J G; Woods G M; Fraser N W
CORPORATE SOURCE: Wistar Institute, Philadelphia, Pennsylvania 19104.
CONTRACT NUMBER: AI-23968 (NIAID)
SOURCE: Journal of virology, **(1991 Dec)** 65 (12) 6800-10.
Journal code: 0113724. ISSN: 0022-538X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M64578; GENBANK-M64579; GENBANK-M64580; GENBANK-M64581; GENBANK-M64582; GENBANK-M64583; GENBANK-M74421; GENBANK-M74720; GENBANK-S59503; GENBANK-S59651
ENTRY MONTH: 199112
ENTRY DATE: Entered STN: 19920124
Last Updated on STN: 19920124
Entered Medline: 19911226

AB Herpes simplex virus type 1 establishes latent infection in trigeminal ganglia of mice infected via the eye. A family of three colinear viral transcripts (LATs), 2.0, 1.5, and 1.45 kb, is present in latently infected ganglia. To characterize these LATs, lambda gt10 cDNA libraries were constructed with RNAs isolated from the trigeminal ganglia of latently infected mice. A series of recombinant **bacteriophage** were isolated containing cDNA inserts covering 1.7 kb of the 2.0-kb LAT. Splice junctions of the smaller LATs and the 3' end of the 2.0-kb LAT were identified by sequence analysis of RNA **polymerase** chain reaction products. No splice acceptor site, which does not support the hypotheses that the 2.0-kb LAT is an intron. However, the data are consistent with the possibility of a short leader sequence or multiple LAT transcription start sites. To generate the smaller 1.5- and 1.45-kb LATs, there is a 559-nucleotide **intron spliced** from the 2.0-kb LAT in strain F and a 556-nucleotide intron in strain 17+. The nucleotide sequences at the 5' and 3' ends of these **introns** are characteristic of **spliced** transcripts from eukaryotic protein-encoding genes, with one significant difference; i.e., the 5' end of the LAT intron is GC instead of the consensus sequence GT. This splice donor sequence is conserved in herpes simplex virus type 1 strains F, 17+, and KOS. Processing of the 2.0-kb LAT to form the spliced LATs preserves two open reading frames (ORFs) at the 3' end of the LATs; no new ORFs are created. Splicing of the LATs positions a 276-nucleotide leader sequence

close to these ORFs and removes an intron that inhibits their translation in vitro. The novel 5' structure of the intron within the 2.0-kb LAT may be part of a control mechanism for transcription processing that results in splicing of the LATs only in sensory neurons during latent infection and reactivation but not during the viral replication cycle.

L26 ANSWER 4 OF 5 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 91355869 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2103447
TITLE: Analysis of the genes encoding the largest subunit of RNA **polymerase** II in Arabidopsis and soybean.
AUTHOR: Dietrich M A; Prenger J P; Guilfoyle T J
CORPORATE SOURCE: Department of Plant Biology, University of Minnesota, St. Paul 55108.
CONTRACT NUMBER: 1 U41 RR-01685-05 (NCRR)
GM37950 (NIGMS)
SOURCE: Plant molecular biology, **(1990 Aug)** 15 (2) 207-23.
Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X52492; GENBANK-X52493; GENBANK-X52494; GENBANK-X52495
ENTRY MONTH: 199110
ENTRY DATE: Entered STN: 19911027
Last Updated on STN: 19970203
Entered Medline: 19911004

AB We have cloned and sequenced the gene encoding the largest subunit of RNA **polymerase** II (RPB1) from Arabidopsis thaliana and partially sequenced genes from soybean (Glycine max). We have also determined the nucleotide sequence for a number of cDNA clones which encode the carboxyl terminal domains (CTDs) of RNA **polymerase** II from both soybean and Arabidopsis. The Arabidopsis RPB1 gene encodes a polypeptide of approximately 205 kDa, consists of 12 exons, and encompasses more than 8 kb. Predicted amino acid sequence shows eight regions of similarity with the largest subunit of other **prokaryotic** and eukaryotic RNA **polymerases**, as well as a highly conserved CTD unique to RNA **polymerase** II. The CTDs in plants, like those in most other eukaryotes, consist of tandem heptapeptide repeats with the consensus amino acid sequence PTSPSYS. The portion of RPB1 which encodes the CTD in plants differs from that of RPB1 of animals and lower eukaryotes. All the plant genes examined contain 2-3 introns within the CTD encoding regions, and at least two plant genes contain an alternatively **spliced intron** in the 3' untranslated region. Several clustered amino acid substitutions in the CTD are conserved in the two plant species examined, but are not found in other eukaryotes. RPB1 is encoded by a multigene family in soybean, but a single gene encodes this subunit in Arabidopsis and most other eukaryotes.

L26 ANSWER 5 OF 5 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 87080257 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2431897
TITLE: Accurate in vitro splicing of two pre-mRNA plant introns in a HeLa cell nuclear extract.
AUTHOR: Brown J W; Feix G; Frendewey D
SOURCE: EMBO journal, **(1986 Nov)** 5 (11) 2749-58.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198702

ENTRY DATE: Entered STN: 19900302
Last Updated on STN: 19970203
Entered Medline: 19870217

AB Two plant introns along with flanking exon sequences have been isolated from an amylase gene of wheat and a legumin gene of pea and cloned behind the phage **SP6** promoter. Pre-mRNAs produced by in vitro transcription with **SP6** RNA **polymerase** were tested for their ability to be spliced in a HeLa cell nuclear extract. The plant **introns** were accurately **spliced** and the predicted splice junctions were used. Lariat RNAs were observed as both intermediates and final products during the splicing reaction. The branch points were mapped to adenosine residues lying within sequences that showed good homology to the animal branch point consensus. Consensus sequences for the 5' and 3' splice junctions and for putative branch point sequences of plants were derived from an analysis of 168 plant intron sequences.

=> d his

(FILE 'HOME' ENTERED AT 11:57:47 ON 01 JUL 2004)

FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 11:57:54 ON 01 JUL 2004

L1 949985 S POLYMERASE?
L2 760 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (2N) L1
L3 2599 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1
L4 5927 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1) OR T3 OT T7 OR S
L5 32470 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) (S) L1) OR T3
L6 275 S L5 (S) INTRON?
L7 448 S L5 (2N) INTRON?
L8 131 DUP REM L6 (144 DUPLICATES REMOVED)
L9 74 S L8 AND PY<=1997
L10 2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L11 2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L12 37 S L5 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSER
L13 16 DUP REM L12 (21 DUPLICATES REMOVED)
L14 11 S L13 AND PY<=1997
L15 1023 S L1 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSERT
L16 3471 S L15 AND ((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L17 107 S L15 AND (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L18 107 S L15 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L19 46 S L17 AND (L1 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTE
L20 28 S L17 AND (L1 (S) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTE
L21 12 DUP REM L20 (16 DUPLICATES REMOVED)
L22 5 S L21 NOT L14
L23 0 S L22 AND PY<=1995
L24 13 S L19 AND PY=<1995
L25 13 S L24 NOT L22
L26 5 DUP REM L25 (8 DUPLICATES REMOVED)
L27 10 S L26 OR L22
L28 10 DUP REM L27 (0 DUPLICATES REMOVED)

=> s l1 (5n) intron?
L29 860 L1 (5N) INTRON?

=> s l29 and (intron (5n) (INTRODUC? OR (NON (2N) NATIV?) OR INSERT? or spliced)
UNMATCHED LEFT PARENTHESIS 'AND (INTRON'
The number of right parentheses in a query must be equal to the number of left parentheses.

=> s l29 and (intron (5n) (INTRODUC? OR (NON (2N) NATIV?) OR INSERT? or spliced))
L30 57 L29 AND (INTRON (5N) (INTRODUC? OR (NON (2N) NATIV?) OR INSERT? OR SPLICED))

```
=> dup rem l30
PROCESSING COMPLETED FOR L30
L31          24 DUP REM L30 (33 DUPLICATES REMOVED)

=> s l31 and py=<1995
   2 FILES SEARCHED...
L32           7 L31 AND PY=<1995

=> d l32 ibib abs 1-7

L32  ANSWER 1 OF 7     MEDLINE on STN
ACCESSION NUMBER:    94063517     MEDLINE
DOCUMENT NUMBER:     PubMed ID: 8244032
TITLE:               Small subunit rDNA variation in a population of lichen
                     fungi due to optional group-I introns.
AUTHOR:              DePriest P T
CORPORATE SOURCE:    Department of Botany, Duke University, Durham, NC
                     27708-0342.
SOURCE:              Gene, (1993 Nov 30) 134 (1) 67-74.
                     Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY:        Netherlands
DOCUMENT TYPE:       Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
ENTRY MONTH:         199401
ENTRY DATE:          Entered STN: 19940201
                     Last Updated on STN: 19990129
                     Entered Medline: 19940105
AB   A natural population of the lichen-forming ascomycetous fungus, Cladonia
     chlorophaea, contained individuals with small subunit ribosomal DNA (SSU
     rDNA) of at least four different size classes and nine restriction-site
     patterns. The source of these differences was the variable occurrence of
     200-400-nucleotide insertions, previously identified as small group-I
     introns, at five different positions within the SSU coding region. By
     specific amplification of the sequences flanking these five intron
     positions with the polymerase chain reaction (PCR), a minimum of
     nine types of rDNA repeats were defined that differ in number, position,
     restriction pattern and size of introns. The positions of the introns
     were verified by sequence analysis. The variable distribution of these
     introns suggests that they are currently mobile--either by intron
     insertion, deletion or both--within this species complex.

L32  ANSWER 2 OF 7     MEDLINE on STN
ACCESSION NUMBER:    92295560     MEDLINE
DOCUMENT NUMBER:     PubMed ID: 1604814
TITLE:               Spliced RNA of woodchuck hepatitis virus.
AUTHOR:              Ogston C W; Razman D G
CORPORATE SOURCE:    Department of Immunology/Microbiology, Rush-Presbyterian-
                     St. Luke's Medical Center, Chicago, Illinois 60612.
SOURCE:              Virology, (1992 Jul) 189 (1) 245-52.
                     Journal code: 0110674. ISSN: 0042-6822.
PUB. COUNTRY:        United States
DOCUMENT TYPE:       Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
OTHER SOURCE:        GENBANK-M90061; GENBANK-M90062
ENTRY MONTH:         199207
ENTRY DATE:          Entered STN: 19920724
                     Last Updated on STN: 19980206
                     Entered Medline: 19920716
AB   Polymerase chain reaction was used to investigate RNA splicing in liver of
     woodchucks infected with woodchuck hepatitis virus (WHV). Two spliced
     species were detected, and the splice junctions were sequenced. The
     larger spliced RNA has an intron of 1300 nucleotides,
```

and the smaller **spliced** sequence shows an additional downstream **intron** of 1104 nucleotides. We did not detect singly **spliced** sequences from which the smaller **intron** alone was removed. Control experiments showed that spliced sequences are present in both RNA and DNA in infected liver, showing that the viral reverse transcriptase can use spliced RNA as template. Spliced sequences were detected also in virion DNA prepared from serum. The upstream intron produces a reading frame that fuses the core to the **polymerase** polypeptide, while the downstream **intron** causes an inframe deletion in the polymerase open reading frame. Whereas the splicing patterns in WHV are superficially similar to those reported recently in hepatitis B virus, we detected no obvious homology in the coding capacity of spliced RNAs from these two viruses.

L32 ANSWER 3 OF 7 MEDLINE on STN
ACCESSION NUMBER: 89083472 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2905037
TITLE: Impairment of yeast pre-mRNA splicing by potential secondary structure-forming sequences near the conserved branchpoint sequence.
AUTHOR: Halfter H; Gallwitz D
CORPORATE SOURCE: Max-Planck-Institute for Biophysical Chemistry, Department of Molecular Genetics, Gottingen, FRG.
SOURCE: Nucleic acids research, **(1988 Nov 25)** 16 (22) 10413-23.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198902
ENTRY DATE: Entered STN: 19900308
Last Updated on STN: 19950206
Entered Medline: 19890203

AB The absolutely conserved TACTAAC box within **introns** of RNA **polymerase** II-transcribed genes of the yeast Saccharomyces cerevisiae serves an indispensable role in lariat formation. We show in this report that rather short palindromic sequences **inserted** into the yeast actin gene **intron** immediately 3' to the TACTAAC box block the second but not the first splicing step. In contrast, a palindromic sequence inserted some 23 bp 3' of the TACTAAC box did not affect correct and efficient splicing. The data suggest that hairpin structures that might form adjacent to the branchsite sequence interfere with some necessary alteration of the spliceosome required for 3' intron cleavage and exon ligation.

L32 ANSWER 4 OF 7 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 93263981 EMBASE
DOCUMENT NUMBER: 1993263981
TITLE: Erythropoietin structure-function relationships: High degree of sequence homology among mammals.
AUTHOR: Wen D.; Boissel J.-P.R.; Tracy T.E.; Gruninger R.H.; Mulcahy L.S.; Czelusniak J.; Goodman M.; Bunn H.F.
CORPORATE SOURCE: Hematology/Oncology Research, LMRC 2, Brigham and Women's Hospital, 221 Longwood Ave,Boston, MA 02115, United States
SOURCE: Blood, (1993) 82/5 (1507-1516).
ISSN: 0006-4971 CODEN: BLOOAW
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 025 Hematology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB To investigate structure-function relationships of erythropoietin (Epo),

we have obtained cDNA sequences that encode the mature Epo protein of a variety of mammals. A first set of primers, corresponding to conserved nucleotide sequences between mouse and human DNAs, allowed us to amplify by **polymerase** chain reaction (PCR) **intron** 1/exon 2 fragments from genomic DNA of the hamster, cat, lion, dog, horse, sheep, dolphin, and pig. Sequencing of these fragments permitted the design of a second generation of species- specific primers. RNA was prepared from anemic kidneys and reverse- transcribed. Using our battery of species-specific 5' primers, we were able to successfully PCR-amplify Epo cDNA from Rhesus monkey, rat, sheep, dog, cat, and pig. Deduced amino acid sequences of mature Epo proteins from these animals, in combination with known sequences for human, Cynomolgus monkey, and mouse, showed a high degree of homology, which explains the biologic and immunological cross-reactivity that has been observed in a number of species. Human Epo is 91% identical to monkey Epo. 85% to cat and dog Epo, and 80% to 82% to pig, sheep, mouse, and rat Epos. There was full conservation of (1) the disulfide bridge linking the NH2 and COOH termini; (2) N-glycosylation sites; and (3) predicted amphipathic α-helices. In contrast, the short disulfide bridge (C29/C33 in humans) is not invariant. Cys33 was replaced by a Pro in rodents. Most of the amino acid replacements were conservative. The C-terminal part of the loop between the C and D helices showed the most variation, with several amino acid substitutions, deletions, and/or **insertions.** Calculations of maximum parsimony for **intron** 1/exon 2 sequences as well as coding sequences enabled the construction of cladograms that are in good agreement with known phylogenetic relationships.

L32 ANSWER 5 OF 7 EMBASE
on STN

ACCESSION NUMBER: 93023448 EMBASE
DOCUMENT NUMBER: 1993023448
TITLE: Chloroplast group III twintron excision utilizing multiple 5'- and 3'-splice sites.
AUTHOR: Copertino D.W.; Shigeoka S.; Hallick R.B.
CORPORATE SOURCE: Dep Molecular and Cellular Biology, University of Arizona,Tucson, AZ 85721, United States
SOURCE: EMBO Journal, (1992) 11/13 (5041-5050).
ISSN: 0261-4189 CODEN: EMJODG
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
022 Human Genetics
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The chloroplast genes of Euglena gracilis contain more than 60 group II and 47 group III introns. Some Euglena chloroplast genes also contain twintrons, introns-within-introns. Two types of twintrons have previously been described, a group II twintron and a mixed group II/group III twintron. We report that four **introns**, three within the RNA **polymerase** subunit gene rpoC1 and one within ribosomal protein gene rpl16, with mean lengths twice typical group III introns, are a new type of twintron. The group III twintrons are composed of group III introns within other group III introns. The splicing of the twintrons was analyzed by PCR amplification, cloning and sequencing of cDNAs, and Northern hybridization. Excision of each group III twintron occurs by a two-step, sequential splicing pathway. Removal of the internal introns precedes excision of the external introns. Splicing of internal introns in three of the four group III twintrons involves multiple 5'- and/or 3'-splice sites. With two of the twintrons the proximal 5'-splice site can be spliced to an internal 3'-splice site, yielding alternative 'pseudo' fully **spliced** mRNAs. Excised group III **introns** of the rpl16 twintron are not linear RNA molecules but either lariat or circular RNAs, probably a lariat. The origins of alternative splicing and a possible evolutionary relationship between group II, group III and nuclear

pre-mRNA introns are discussed.

L32 ANSWER 6 OF 7 CA COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 118:228988 CA
TITLE: The DNA polymerase gene from Chlorella viruses PBCV-1 and NY-2A contains an intron with nuclear splicing sequences
AUTHOR(S): Grabherr, Reingard; Strasser, Peter; Van Etten, James L.
CORPORATE SOURCE: Dep. Plant Pathol., Univ. Nebraska, Lincoln, NE, 68583-0722, USA
SOURCE: Virology (**1992**), 188(2), 721-31
CODEN: VIRLAX; ISSN: 0042-6822
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The deduced amino acid sequences of two eukaryotic chlorella virus (PBCV-1 and NY-2A) DNA polymerases are 90% identical and contain amino acid motifs typical of α-like (Family B) DNA polymerases. The open reading frames of both PBCV-1 and NY-2A DNA polymerases are interrupted by an identically located, small (101 or 86 nucleotides, resp.) **intron** that resembles eukaryotic nuclear-**spliced** mRNA **introns** . This discovery suggests that chlorella virus replication has a nuclear phase.

L32 ANSWER 7 OF 7 CA COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 114:1450 CA
TITLE: The discovery of new intron-containing human tRNA genes using the polymerase chain reaction
AUTHOR(S): Green, Christopher J.; Sohel, Indira; Vold, Barbara S.
CORPORATE SOURCE: SRI Int., Menlo Park, CA, 94025, USA
SOURCE: Journal of Biological Chemistry (**1990**), 265(21), 12139-42
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Introns in tRNA genes are rare in vertebrates. Until now, the only intron-containing human tRNA genes were believed to be those coding for tRNATyr. All of these **introns** are **inserted** 3' to the anticodon position in these genes. Polymerase chain reaction primers were designed that can amplify all of the tRNATyr genes for cloning and sequencing by using the conserved portions of the gene coding for the structural part of the tRNA. Preliminary results have revealed 5 tRNATyr genes, each of which contains a different intron. The same technique was used to amplify, clone, and sequence the human genes for tRNALeuCAA. This has resulted in the discovery that this human tRNA gene family also has **introns inserted** 3' to the anticodon. This polymerase chain reaction technique is useful in detecting new families of intron-containing tRNA genes as well as identifying sequence variations in the introns of individual genes.

=> d his

(FILE 'HOME' ENTERED AT 11:57:47 ON 01 JUL 2004)

FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 11:57:54 ON 01 JUL 2004

L1 949985 S POLYMERASE?
L2 760 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (2N) L1
L3 2599 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1
L4 5927 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1) OR T3 OT T7 OR S
L5 32470 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) (S) L1) OR T3
L6 275 S L5 (S) INTRON?
L7 448 S L5 (2N) INTRON?

```
L8          131 DUP REM L6 (144 DUPLICATES REMOVED)
L9           74 S L8 AND PY<=1997
L10        2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L11        2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L12          37 S L5 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSER
L13          16 DUP REM L12 (21 DUPLICATES REMOVED)
L14          11 S L13 AND PY<=1997
L15        1023 S L1 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSERT
L16        3471 S L15 AND ((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L17         107 S L15 AND (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L18         107 S L15 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L19          46 S L17 AND (L1 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTE
L20          28 S L17 AND (L1 (S) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTE
L21          12 DUP REM L20 (16 DUPLICATES REMOVED)
L22           5 S L21 NOT L14
L23           0 S L22 AND PY<=1995
L24          13 S L19 AND PY=<1995
L25          13 S L24 NOT L22
L26           5 DUP REM L25 (8 DUPLICATES REMOVED)
L27          10 S L26 OR L22
L28          10 DUP REM L27 (0 DUPLICATES REMOVED)
L29         860 S L1 (5N) INTRON?
L30          57 S L29 AND (INTRON (5N) (INTRODUC? OR (NON (2N) NATIV?) OR INSE
L31          24 DUP REM L30 (33 DUPLICATES REMOVED)
L32           7 S L31 AND PY=<1995

=> s l1 (s) intron?
L33        7656 L1 (S) INTRON?

=> s l33 and (INTRON (5N) (INTRODUC? OR (NON (2N) NATIV?) OR INSErt or spliced))
L34         181 L33 AND (INTRON (5N) (INTRODUC? OR (NON (2N) NATIV?) OR INSERT
                OR SPLICED))

=> s l33 and (INTRON (5N) (INTRODUC? OR (NON (2N) NATIV?) OR INSErt? or spliced))
L35         516 L33 AND (INTRON (5N) (INTRODUC? OR (NON (2N) NATIV?) OR INSERT?
                 OR SPLICED))

=> dup rem l35
PROCESSING COMPLETED FOR L35
L36          221 DUP REM L35 (295 DUPLICATES REMOVED)

=> s l36 and py=<1995
   2 FILES SEARCHED...
L37          81 L36 AND PY=<1995

=>

=> s l37 and (polymeras? (s) ((NON (N) EU!ARYOT?) OR PRO!ARYOT? or bacteri? OR T3
OT T7 OR Sp6))
L38           2 L37 AND (POLYMERAS? (S) ((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR
                BACTERI? OR T3 OT T7 OR SP6))

=> d l38 1-2 ibib abs

L38  ANSWER 1 OF 2      MEDLINE on STN
ACCESSION NUMBER:    96069407      MEDLINE
DOCUMENT NUMBER:     PubMed ID: 8524264
TITLE:               Cotranscriptional splicing of a group I intron is
                     facilitated by the Cbp2 protein.
AUTHOR:              Lewin A S; Thomas J Jr; Tirupati H K
CORPORATE SOURCE:    Department of Molecular Genetics and Microbiology,
                     University of Florida College of Medicine, Gainesville
                     32610-0266, USA.
CONTRACT NUMBER:     GM12228 (NIGMS)
```

SOURCE: Molecular and cellular biology, **(1995 Dec)** 15 (12) 6971-8.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199601
ENTRY DATE: Entered STN: 19960219
Last Updated on STN: 20030202
Entered Medline: 19960119

AB The nuclear CBP2 gene encodes a protein essential for the splicing of a mitochondrial group I intron in Saccharomyces cerevisiae. This **intron** (bI5) is **spliced** autocatalytically in the presence of high concentrations of magnesium and monovalent salt but requires the Cbp2 protein for splicing under physiological conditions. Addition of Cbp2 during RNA synthesis permitted cotranscriptional splicing. Splicing did not occur in the transcription buffer in the absence of synthesis. The Cbp2 protein appeared to modify the folding of the **intron** during RNA synthesis: pause sites for RNA **polymerase** were altered in the presence of the protein, and some mutant transcripts that did not splice after transcription did so during transcription in the presence of Cbp2. Cotranscriptional splicing also reduced hydrolysis at the 3' splice junction. These results suggest that Cbp2 modulates the sequential folding of the ribozyme during its synthesis. In addition, splicing during transcription led to an increase in RNA synthesis with both T7 RNA polymerase and mitochondrial RNA polymerase, implying a functional coupling between transcription and splicing.

L38 ANSWER 2 OF 2 EMBASE
on STN
ACCESSION NUMBER: 92022310 EMBASE
DOCUMENT NUMBER: 1992022310
TITLE: Identification of a novel latency-specific splice donor signal within the herpes simplex virus type 1 2.0-kilobase latency-associated transcript (LAT): translation inhibition of LAT open reading frames by the intron within the 2.0-kilobase LAT.
AUTHOR: Spivack J.G.; Woods G.M.; Fraser N.W.
CORPORATE SOURCE: The Wistar Institute, 36th Street at Spruce, Philadelphia, PA 19104, United States
SOURCE: Journal of Virology, (1991) 65/12 (6800-6810).
ISSN: 0022-538X CODEN: JOVIAM
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Herpes simplex virus type 1 establishes latent infection in trigeminal ganglia of mice infected via the eye. A family of three collinear viral transcripts (LATs), 2.0, 1.5, and 1.45 kb, is present in latently infected ganglia. To characterize these LATs, λgt10 cDNA libraries were constructed with RNAs isolated from the trigeminal ganglia of latently infected mice. A series of recombinant **bacteriophage** were isolated containing cDNA inserts covering 1.7 kb of the 2.0-kb LAT. Splice junctions of the smaller LATs and the 3' end of the 2.0-kb LAT were identified by sequence analysis of RNA **polymerase** chain reaction products. No splice was detected in the 2.0-kb LAT. The 3' end of the 2.0-kb LAT in vivo is upstream of a consensus splice acceptor site, which does not support the hypotheses that the 2.0-kb LAT is an **intron**. However, the data are consistent with the possibility of a short leader sequence or multiple LAT transcription start sites. To generate the smaller 1.5- and 1.45-kb LATs, there is a 559-nucleotide **intron**

spliced from the 2.0-kb LAT in strain F and a 556-nucleotide **intron** in strain 17+. The nucleotide sequences at the 5' and 3' ends of these **introns** are characteristic of **spliced** transcripts from eukaryotic protein-encoding genes, with one significant difference; i.e., the 5' end of the LAT **intron** is GC instead of the consensus sequence GT. This splice donor sequence is conserved in herpes simplex virus type 1 strains F, 17+, and KOS. Processing of the 2.0-kb LAT to form the spliced LATs preserves two open reading frames (ORFs) at the 3' end of the LATs; no new ORFs are created. Splicing of the LATs positions a 276-nucleotide leader sequence close to these ORFs and removes an **intron** that inhibits their translation in vitro. The novel 5' structure of the **intron** within the 2.0-kb LAT may be part of a control mechanism for transcription processing that results in splicing of the LATs only in sensory neurons during latent infection and reactivation but not during the viral replication cycle.

```
=> d his

     (FILE 'HOME' ENTERED AT 11:57:47 ON 01 JUL 2004)

     FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 11:57:54 ON 01
     JUL 2004
L1        949985 S POLYMERASE?
L2           760 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (2N) L1
L3          2599 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1
L4          5927 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1) OR T3 OT T7 OR S
L5         32470 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) (S) L1) OR T3
L6           275 S L5 (S) INTRON?
L7           448 S L5 (2N) INTRON?
L8           131 DUP REM L6 (144 DUPLICATES REMOVED)
L9            74 S L8 AND PY<=1997
L10         2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L11         2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L12           37 S L5 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSER
L13           16 DUP REM L12 (21 DUPLICATES REMOVED)
L14           11 S L13 AND PY<=1997
L15         1023 S L1 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSERT
L16         3471 S L15 AND ((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L17          107 S L15 AND (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L18          107 S L15 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L19           46 S L17 AND (L1 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTE
L20           28 S L17 AND (L1 (S) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTE
L21           12 DUP REM L20 (16 DUPLICATES REMOVED)
L22            5 S L21 NOT L14
L23            0 S L22 AND PY<=1995
L24           13 S L19 AND PY=<1995
L25           13 S L24 NOT L22
L26            5 DUP REM L25 (8 DUPLICATES REMOVED)
L27           10 S L26 OR L22
L28           10 DUP REM L27 (0 DUPLICATES REMOVED)
L29          860 S L1 (5N) INTRON?
L30           57 S L29 AND (INTRON (5N) (INTRODUC? OR (NON (2N) NATIV?) OR INSE
L31           24 DUP REM L30 (33 DUPLICATES REMOVED)
L32            7 S L31 AND PY=<1995
L33         7656 S L1 (S) INTRON?
L34          181 S L33 AND (INTRON (5N) (INTRODUC? OR (NON (2N) NATIV?) OR INSE
L35          516 S L33 AND (INTRON (5N) (INTRODUC? OR (NON (2N) NATIV?) OR INSE
L36          221 DUP REM L35 (295 DUPLICATES REMOVED)
L37           81 S L36 AND PY=<1995
L38            2 S L37 AND (POLYMERAS? (S) ((NON (N) EU!ARYOT?) OR PRO!ARYOT? O

=> s l37 not (l32 or l26 or l14)
L39           74 L37 NOT (L32 OR L26 OR L14)
```

=> s l39 and (polymeras? (5n) ((NON (N) EU!ARYOT?) OR PRO!ARYOT? or bacteri? OR T3 OT T7 OR Sp6))
3 FILES SEARCHED...
L40 0 L39 AND (POLYMERAS? (5N) ((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTERI? OR T3 OT T7 OR SP6))

=> d l39 ibib abs 1-5

L39 ANSWER 1 OF 74 MEDLINE on STN
ACCESSION NUMBER: 96123430 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8596437
TITLE: Mutational analysis reveals dispensability of the N-terminal region of the Aspergillus transcription factor mediating nitrogen metabolite repression.
COMMENT: Erratum in: Mol Microbiol 1996 Apr;20(1):239
AUTHOR: Langdon T; Sheerins A; Ravagnani A; Gielkens M; Caddick M X; Arst H N Jr
CORPORATE SOURCE: Department of Infectious Diseases and Bacteriology, Royal Postgraduate Medical School, London, UK.
SOURCE: Molecular microbiology, **(1995 Sep)** 17 (5) 877-88. Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X52491
ENTRY MONTH: 199604
ENTRY DATE: Entered STN: 19960424
Last Updated on STN: 20021210
Entered Medline: 19960417

AB Mutational analysis has enabled identification and localization of an upstream exon of the areA gene of Aspergillus nidulans mediating nitrogen metabolite repression. A mutation in the initiation codon and frameshift mutations, which revert by restoration of the reading frame, established the coding role of the exon and mutations affecting **intron** splicing in conjunction with DNA sequencing of reverse transcriptase **polymerase** chain reaction (RT-PCR) products localized the coding region **intron.** The resulting AREA translation product would have 876 residues. Deletion of the upstream exon such that translation of the remaining areA coding region would yield a protein containing only the 719 C-terminal residues has only a subtle phenotype, very similar to those resulting from single amino acid replacements in upstream exon-encoded regions of strong sequence similarity to the Neurospora crassa and Penicillium chrysogenum homologues. A number of areA mRNAs of different sizes are synthesised and appear to be functionally redundant. Synthesis of at least the smallest mRNA(s) is probably subject to autogenous activation. Suppression of frameshift mutations by compensating mutations preventing **intron** splicing suggests that **insertion** of a markedly hydrophobic sequence can impair AREA function. Finally, translational initiation for areA can occur within a region of at least 123 nucleotides.

L39 ANSWER 2 OF 74 MEDLINE on STN
ACCESSION NUMBER: 96114734 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7492954
TITLE: Evidence that polymorphism of the angiotensin I converting enzyme gene may be related to idiopathic dilated cardiomyopathy in the Chinese population.
AUTHOR: Harn H J; Chang C Y; Ho L I; Liu C A; Jeng J R; Lin F G; Jent-Wei
CORPORATE SOURCE: Department of Pathology, Tri-Service General Hospital, Taipei, Taiwan.
SOURCE: Biochemistry and molecular biology international,

(1995 May) 35 (6) 1175-81.
Journal code: 9306673. ISSN: 1039-9712.
PUB. COUNTRY: Australia
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199601
ENTRY DATE: Entered STN: 19960217
Last Updated on STN: 19990129
Entered Medline: 19960111

AB Angiotensin I-converting enzyme (ACE) is responsible for the production of angiotension II and the breakdown of kinins, leading to increased blood pressure (BP), induction of vascular smooth muscle cell proliferation, and the stimulation of myocardial-cell hypertrophy. A 287 bp **insertion**/deletion polymorphism in **intron** 16 of the ACE gene was examined by **polymerase** chain reaction in a cross-sectional study of 35 patients with idiopathic dilated cardiomyopathy (IDC) and 35 patients with normally functioning hearts (NT). Compared with the deletion/deletion (D/D) frequency in the control population, the frequency of the deletion allele was 0.757 in IDC patients and 0.600 in NTs; the difference between observed alleles in all subjects in each group was significant ($x2 = 3.96$; $P < 0.05$). The data thus provide evidence in favor of an association between idiopathic dilated cardiomyopathy and a polymorphism at the ACE locus (17q23), thus implicating this locus, and possibly a genetic variant of ACE, itself, in human idiopathic dilated cardiomyopathy.

L39 ANSWER 3 OF 74 MEDLINE on STN
ACCESSION NUMBER: 95290024 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7772074
TITLE: A deletion polymorphism in the angiotensin converting enzyme gene is not associated with coronary heart disease in an Austrian population.
AUTHOR: Friedl W; Krempler F; Paulweber B; Pichler M; Sandhofer F
CORPORATE SOURCE: Rehabilitation Center Grossgmain, Salzburg, Austria.
SOURCE: Atherosclerosis, **(1995 Jan 20)** 112 (2) 137-43.
Journal code: 0242543. ISSN: 0021-9150.
PUB. COUNTRY: Ireland
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199507
ENTRY DATE: Entered STN: 19950713
Last Updated on STN: 19950713
Entered Medline: 19950706

AB This study examined a possible relationship between genetic variation in the gene coding for the angiotensin converting enzyme (ACE) and increased risk for coronary heart disease (CHD) in an Austrian population. **Polymerase** chain reaction (PCR) was used to determine the genotypes for an **insertion**/deletion polymorphism in **intron** 16 of the ACE gene in 315 patients with CHD and in 149 normal controls. In the control group, the relative allele frequencies of the polymorphism were similar to those of previously published European studies. The genotype distribution among our patients was not significantly different from that among controls. We were not able to show a significant association of the DD genotype with coronary heart disease in subgroups containing patients considered at low coronary risk. There was no association of lipid parameters and ACE genotype. From these data we conclude that, in the Austrian population, the insertion/deletion polymorphism in the ACE gene cannot be used as a marker for coronary risk assessment.

L39 ANSWER 4 OF 74 MEDLINE on STN
ACCESSION NUMBER: 95257467 MEDLINE

DOCUMENT NUMBER: PubMed ID: 7739115
TITLE: Deletion polymorphism of the angiotensin I-converting enzyme gene associates with increased risk for ischemic heart diseases in the Japanese.
AUTHOR: Nakai K; Itoh C; Miura Y; Nakai K; Syo T; Musya T; Hiramori K
CORPORATE SOURCE: 2nd Department of Internal Medicine, Iwate Medical University, Morioka.
SOURCE: Rinsho byori. Japanese journal of clinical pathology, **(1995 Apr)** 43 (4) 347-52.
Journal code: 2984781R. ISSN: 0047-1860.
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: Japanese
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199506
ENTRY DATE: Entered STN: 19950615
Last Updated on STN: 19950615
Entered Medline: 19950607

AB The Angiotensin I-converting enzyme (ACE) is a key component of the renin-angiotensin system thought to be important in the pathogenesis of hypertension and cardiovascular diseases. Previous studies showed that deletion polymorphism in the the ACE gene might be a risk factor for myocardial infarction in the Caucasian population, but, this finding has not yet been reported in a Japanese population. In this study, a 287 base pair (bp) **insertion**/deletion polymorphism in **intron** 16 of the ACE gene was examined by the **polymerase** chain reaction (PCR) in a cross-sectional study of 100 healthy subjects and 218 patients with ischemic heart diseases (IHD) (70 angina pectoris, 148 myocardial infarction). Polymorphism of the ACE gene was characterized by three genotypes: two deletion alleles (genotype DD), two insertion allele (genotype II) and heterozygotes alleles (genotype ID). No differences could be detected among the three genotypes for total cholesterol, high-density lipoprotein cholesterol, blood pressure and body mass index. The serum ACE activity in each II, ID and DD genotype was 11.4 +/- 2:7 microU/ml, 14.5 +/- 3.5 microU/ml, 16.6 +/- 4.6 microU/ml, respectively. In the population study, genotype DD was significantly associated with IHD when compared with the other two genotypes (ID and II). The frequency of deletion allele was higher (0.56) in the IHD group than in the normal individuals (0.42) ($p < 0.05$). These frequencies were not varied whether they had classic risk factors or not. Furthermore, coronary multivessel impairment was significantly associated with a deletion allele than with an insertion allele ($p < 0.01$).(ABSTRACT TRUNCATED AT 250 WORDS)

L39 ANSWER 5 OF 74 MEDLINE on STN
ACCESSION NUMBER: 95189102 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7883184
TITLE: A group-I intron in the mitochondrial large-subunit ribosomal RNA-encoding gene of Dictyostelium discoideum: same site localization in alga and in vitro self-splicing.
AUTHOR: Angata K; Ogawa S; Yanagisawa K; Tanaka Y
CORPORATE SOURCE: Institute of Biological Sciences, University of Tsukuba, Ibaraki, Japan.
SOURCE: Gene, **(1995 Feb 3)** 153 (1) 49-55.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-D16466; GENBANK-J01427; GENBANK-V00684; GENBANK-X06961; GENBANK-X14735; GENBANK-X17375; GENBANK-X68722
ENTRY MONTH: 199504
ENTRY DATE: Entered STN: 19950425

Last Updated on STN: 19990129
Entered Medline: 19950407

AB A 547-bp group-I intron belonging to subgroup IA1 was found near the 3' end of the large subunit ribosomal RNA-encoding gene (LSUrRNA) in the mitochondrial (mt) DNA of the cellular slime mold Dictyostelium discoideum. This **intron** was **inserted** in a highly conserved stretch within the sequence that encodes the peptidyl transferase center domain V in the corresponding region of the Escherichia coli LSUrRNA. Interestingly, the **insertion** site of the **intron** is the same as that of the So.LSU.2 intron of the green alga, Scenedesmus obliquus, mt DNA and the Pw.LSU.2 intron of the colorless alga, Prototheca wickerhamii, mt DNA. The intron could self-splice in vitro at a concentration higher than 20 mM MgCl2. **Polymerase** chain reaction analysis showed the possible existence of an **intron** similar to that of D. discoideum LSUrRNA in another cellular slime mold, Polysphondylium pallidum (CK-8), but not in D. mucoroides (Dm7 and Dm11).

=> d his

(FILE 'HOME' ENTERED AT 11:57:47 ON 01 JUL 2004)

FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 11:57:54 ON 01 JUL 2004

L1 949985 S POLYMERASE?
L2 760 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (2N) L1
L3 2599 S ((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1
L4 5927 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT?) (S) L1) OR T3 OT T7 OR S
L5 32470 S (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) (S) L1) OR T3
L6 275 S L5 (S) INTRON?
L7 448 S L5 (2N) INTRON?
L8 131 DUP REM L6 (144 DUPLICATES REMOVED)
L9 74 S L8 AND PY<=1997
L10 2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L11 2322 S L5 AND (INTRON (3N) (INTRODUC? OR NON (2N) NATIV?) OR INSERT
L12 37 S L5 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSER
L13 16 DUP REM L12 (21 DUPLICATES REMOVED)
L14 11 S L13 AND PY<=1997
L15 1023 S L1 AND (INTRON (3N) ((INTRODUC? OR NON (2N) NATIV?) OR INSERT
L16 3471 S L15 AND ((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L17 107 S L15 AND (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L18 107 S L15 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTER?) OR T3
L19 46 S L17 AND (L1 (P) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTE
L20 28 S L17 AND (L1 (S) (((NON (N) EU!ARYOT?) OR PRO!ARYOT? OR BACTE
L21 12 DUP REM L20 (16 DUPLICATES REMOVED)
L22 5 S L21 NOT L14
L23 0 S L22 AND PY<=1995
L24 13 S L19 AND PY=<1995
L25 13 S L24 NOT L22
L26 5 DUP REM L25 (8 DUPLICATES REMOVED)
L27 10 S L26 OR L22
L28 10 DUP REM L27 (0 DUPLICATES REMOVED)
L29 860 S L1 (5N) INTRON?
L30 57 S L29 AND (INTRON (5N) (INTRODUC? OR (NON (2N) NATIV?) OR INSE
L31 24 DUP REM L30 (33 DUPLICATES REMOVED)
L32 7 S L31 AND PY=<1995
L33 7656 S L1 (S) INTRON?
L34 181 S L33 AND (INTRON (5N) (INTRODUC? OR (NON (2N) NATIV?) OR INSE
L35 516 S L33 AND (INTRON (5N) (INTRODUC? OR (NON (2N) NATIV?) OR INSE
L36 221 DUP REM L35 (295 DUPLICATES REMOVED)
L37 81 S L36 AND PY=<1995
L38 2 S L37 AND (POLYMERAS? (S) ((NON (N) EU!ARYOT?) OR PRO!ARYOT? O
L39 74 S L37 NOT (L32 OR L26 OR L14)

L40 0 S L39 AND (POLYMERAS? (5N) ((NON (N) EU!ARYOT?) OR PRO!ARYOT?

=> s l39 not ((polymerase chain reaction) or PCR)
L41 5 L39 NOT ((POLYMERASE CHAIN REACTION) OR PCR)

=> d l41 1-5 ibib abs

L41 ANSWER 1 OF 5 MEDLINE on STN
ACCESSION NUMBER: 92263776 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1585643
TITLE: The DNA **polymerase** gene from chlorella viruses PBCV-1 and NY-2A contains an **intron** with nuclear splicing sequences.
AUTHOR: Grabherr R; Strasser P; Van Etten J L
CORPORATE SOURCE: Department of Plant Pathology, University of Nebraska, Lincoln 68583-0722.
CONTRACT NUMBER: GM-32441 (NIGMS)
SOURCE: Virology, **(1992 Jun)** 188 (2) 721-31.
Journal code: 0110674. ISSN: 0042-6822.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M86836; GENBANK-M86837
ENTRY MONTH: 199206
ENTRY DATE: Entered STN: 19920626
Last Updated on STN: 19980206
Entered Medline: 19920617

AB The deduced amino acid sequences of two eukaryotic chlorella virus (PBCV-1 and NY-2A) DNA polymerases are 90% identical and contain amino acid motifs typical of alpha-like (Family B) DNA polymerases. The open reading frames of both PBCV-1 and NY-2A DNA **polymerases** are interrupted by an identically located, small (101 or 86 nucleotides, respectively) **intron** that resembles eukaryotic nuclear-**spliced** messenger RNA **introns.** This discovery suggests that chlorella virus replication has a nuclear phase.

L41 ANSWER 2 OF 5 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 92356435 EMBASE
DOCUMENT NUMBER: 1992356435
TITLE: Characterization of the self-splicing products of a mobile intron from the nuclear rDNA of Physarum polycephalum.
AUTHOR: Ruoff B.; Johansen S.; Vogt V.M.
CORPORATE SOURCE: Section of Biochemistry, Molecular and Cell Biology, Cornell University,Ithaca, NY 14853, United States
SOURCE: Nucleic Acids Research, (1992) 20/22 (5899-5906).
ISSN: 0305-1048 CODEN: NARHAD
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
022 Human Genetics
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We have characterized the splicing products formed in vitro from RNA derived from the mobile group I **intron** in the nuclear rDNA of Physarum polycephalum, Pp LSU 3. This **intron** is a close relative of the well known Tetrahymena **intron** Tt LSU 1, being **inserted** at exactly the same position in the rDNA and sharing about 90% sequence identity with Tt LSU 1 in the conserved elements characteristic of the catalytic core of all group I **introns.** However, Pp LSU 3 differs from Tt LSU 1 in that it encodes a site-specific endonuclease, which mediates the homing of the **intron** to unoccupied target sites. The endonuclease, I-Ppo, would appear to be a

unique example of a protein encoded by an RNA **polymerase** I transcript. To gain clues to the splicing products formed in vivo, and to the nature of the messenger RNA for I-Ppo, we subjected Pp LSU 3 RNA to standard self-splicing conditions in vitro, and then analyzed the products by size, by northern blotting, and by primer extension. The results show two novel features. First, in addition to the expected 5' splice site, there is an alternative 5' splice site in the upstream exon, just preceding the first codon of the I-Ppo open reading frame. Second, at the position corresponding to the major circularization site in Tt LSU 1 there is an internal processing site, leading to the efficient separation of two halves of the excised **intron**, the 5' half encoding I-Ppo and 3' half containing the ribozyme. Surprisingly, this cleavage appears not to be due to circularization followed by hydrolytic opening of the circle, but rather to G addition. The formation of these products in vitro suggests how the messenger RNA for the I-Ppo endonuclease may be generated in vivo.

L41 ANSWER 3 OF 5 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 91056142 EMBASE
DOCUMENT NUMBER: 1991056142
TITLE: Recombinations between Alu repeat sequences that result in partial deletions within the C1 inhibitor gene.
AUTHOR: Ariga T.; Carter P.E.; Davis III. A.E.
CORPORATE SOURCE: Department of Pediatrics, Hokkaido University School of Medicine, Sapporo, Japan
SOURCE: Genomics, (1990) 8/4 (607-613).
ISSN: 0888-7543 CODEN: GNMCEP
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Genomic DNA sequence analysis was used to define the extent of deletions within the C1 inhibitor gene in two families with type I hereditary angioneurotic edema. Southern blot analysis initially indicated the presence of the partial deletions. One deletion was approximately 2 kb and included exon VII, whereas the other was approximately 8.5 kb and included exons IV-VI. Genomic libraries from an affected member of each family were constructed and clones containing the deletions were analyzed. Sequence analysis of the deletion joints of the mutants and corresponding regions of the normal gene in the two families demonstrated that both deletion joints resulted from recombination of two Alu repetitive DNA elements. Alu repeat sequences from **introns** VI and VII combined to make a novel Alu in family A, and Alu sequences in **introns** III and VI were **spliced** to make a new Alu in family B. The splice sites in the Alu sequences of both mutants were located in the left arm of the Alu element, and both recombination joints overlapped one of the RNA **polymerase** III promoter sequences. Because the involved Alu sequences, in both instances, were oriented in the same direction, unequal crossingover is the most likely mechanism to account for these mutations.

L41 ANSWER 4 OF 5 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 90196215 EMBASE
DOCUMENT NUMBER: 1990196215
TITLE: Nucleotide sequence of the maize chloroplast rpo B/C1/C2 operon: Comparison between the derived protein primary structures from various organisms with respect to functional domains.
AUTHOR: Igloi G.L.; Meinke A.; Dory I.; Kossel H.
CORPORATE SOURCE: Institut fur Biologie III, Universitat Freiburg, Schanzlestrasse 1,D-7800 Freiburg, Germany

SOURCE: Molecular and General Genetics, (1990) 221/3 (379-394).
ISSN: 0026-8925 CODEN: MGGEAE
COUNTRY: Germany
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 022 Human Genetics
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The genes (rpo B/C1/C2) coding for the β, β', β'' subunits of maize (Zea mays) chloroplast RNA **polymerase** have been located on the plastome and their nucleotide sequences established. The operon is part of a large inversion with respect to the tobacco and spinach chloroplast genomes and is flanked by the genes trnC and rps2. Notable features of the nucleotide sequence are the loss of an **intron** in rpoC1 and an **insertion** of approximately 450 bp in rpoC2 compared to the dicotyledons tobacco, spinach and liverwort. The derived amino acid sequence of this additional monocotyledon specific sequence is characterized by acidic heptameric repeat units containing stretches of glutamic acid, tyrosines and leucines with regular spacing. Other structural motifs, such as a nucleotide binding domain in the β subunit and a zinc finger in the β' subunit, are compared at the amino acid level throughout the RNA **polymerase** subunits with the enzymes from other organisms in order to identify functionally important conserved regions.

L41 ANSWER 5 OF 5 CA COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 116:35640 CA
TITLE: New diagnostic and treatment methods involving the cystic fibrosis transmembrane regulator
INVENTOR(S): Gregory, Richard J.; Cheng, Seng H.; Smith, Alan; Paul, Sucharita; Hehir, Kathleen M.; Marshall, John
PATENT ASSIGNEE(S): Genzyme Corp., USA
SOURCE: Eur. Pat. Appl., 49 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 7
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 446017	A1	19910911	EP 1991-301819	19910305 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				
CA 2037478	AA	19910906	CA 1991-2037478	19910304 <--
JP 06303978	A2	19941101	JP 1991-38810	19910305 <--
US 5981714	A	19991109	US 1996-691605	19960815
US 5750571	A	19980512	US 1996-774127	19961223
US 2002164782	A1	20021107	US 2000-568756	20000511
AU 765709	B2	20030925	AU 2000-53512	20000821
US 2003147854	A1	20030807	US 2002-161539	20020603

PRIORITY APPLN. INFO.:
US 1990-488307 A 19900305
US 1990-589295 A 19900927
US 1990-613592 A 19901115
US 1992-935603 B2 19920826
US 1992-985478 B2 19921203
US 1993-72708 A1 19930607
US 1993-87132 A2 19930702
AU 1997-43655 A3 19971031
US 1998-114950 B1 19980827
US 1999-248026 A1 19990210
US 2000-568756 B1 20000511

AB A cDNA for the complete human cystic fibrosis transmembrane conductance regulator (CFTCR) is provided. A method for stabilizing CFTER clones comprises placing it in a low-copy number plasmid, **inserting** an

intron into the coding sequence, and/or altering the sequence to remove cryptic RNA **polymerase** promoter sequences. The CFTCR cDNA can be used to produce the CFTCR, to treat cystic fibrosis, to prepare transgenic animals, and to diagnose CFTCR dysfunction. Many mutations known to occur in cystic fibrosis patients were introduced into CFTCR cDNA, and this mutant cDNA was expressed in COS-7 cells. The mutations Δ phenylalanine-508, Δ isoleucine-507, lysine-464 changes to methionine, phenylalanine-508 changed to arginine, and serine-549 changed to isoleucine resulted in production of unstable, incompletely glycosylated CFTCR.

=>

---Logging off of STN---

=>
Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	443.76	443.97
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-3.30	-3.30

STN INTERNATIONAL LOGOFF AT 13:26:29 ON 01 JUL 2004

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:ssspta1635jxs

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * * * Welcome to STN International * * * * * * * * * *

NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2		"Ask CAS" for self-help around the clock
NEWS 3	May 10	PROUSDDR now available on STN
NEWS 4	May 19	PROUSDDR: One FREE connect hour, per account, in both May and June 2004
NEWS 5	May 12	EXTEND option available in structure searching
NEWS 6	May 12	Polymer links for the POLYLINK command completed in REGISTRY
NEWS 7	May 17	FRFULL now available on STN
NEWS 8	May 27	New UPM (Update Code Maximum) field for more efficient patent SDIs in CAplus
NEWS 9	May 27	CAplus super roles and document types searchable in REGISTRY
NEWS 10	May 27	Explore APOLLIT with free connect time in June 2004
NEWS 11	Jun 22	STN Patent Forums to be held July 19-22, 2004